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(54) Title: OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE

(57) Abstract: The present invention relates to olfactory receptor genes and pseudogenes of 10 primate species, in addition to mouse. The invention also concerns olfactory receptors encoded by these genes and their utilization.

OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE

5 The present invention relates to the discovery
of olfactory receptor genes and pseudogenes in primates and
mouse, the olfactory receptors encoded by these genes and
their utilization.

10 Mammals are able to discriminate between
thousands of odour molecules. This capacity relies on a
multigene family encoding 500 - 1000 olfactory receptors
(OR) (1). These receptors are expressed mainly in the
olfactory epithelium and have been found in a number of
species including mammals (1-5), birds (6, 7), amphibians
(8) and fish (9). All these receptors belong to the G
15 protein-coupled receptor (GPCR) superfamily and share
features of sequence and structure, such as seven
hydrophobic transmembrane domains (7TM).

20 The sense of smell plays an important role in
mammalian social behavior, location of food and detection of
predators. However, mammals vary in their olfactory ability
(10, 11). The sense of smell in primates is greatly reduced
(microsmatic) with respect to other mammals such as dogs
(12) or rodents (10, 11). Various explanations for the
differences in olfactory performance have been hypothesized.
25 Differences in the anatomical structures (size, location)
devoted to olfaction could partly explain these differences.
For example, dogs, which have an olfactory sensitivity up to
100 times greater than humans, have on average ~100 cm² of
olfactory epithelium whilst humans have only 10 cm² ((4) and
30 references therein). Variations in the size and diversity of
the expressed OR gene family could also account for these
differences. The Applicant recently demonstrated that the
human OR gene repertoire is distributed in over 25
chromosomal sites, and over 70% of these OR genes are
35 pseudogenes, i.e. the sequences have accumulated deleterious
mutations such as in-frame stop codons and/or indel
frameshifts (3). This finding led us to hypothesize that the
reduction of the sense of smell observed in primates could
parallel the reduction of the number of functional OR genes.

In order to test this hypothesis the Applicant wished to characterize the evolution of the OR gene family in other primates. A random survey of OR genes from primate hominoids to prosimians was performed. In parallel, a mouse OR-enriched library from genomic DNA in order to sequence a number of OR was constructed. The comparison of the OR gene repertoire from macrosmatic mouse and primates provides insight into the evolution of this multigene family and could reflect the evolution of a sensory function in mammals in response to selective constraints.

The invention thus concerns a molecule of nucleic acid constituted by or comprising a sequence chosen among those represented in the list of sequences in the appendix under the numbers SEQ ID No. 3, SEQ ID No. 12, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 52, SEQ ID No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID No. 60, SEQ ID No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 120, SEQ ID No. 121, SEQ ID No. 122, SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEQ ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 233, SEQ ID No. 238, SEQ ID No. 239, SEQ ID No. 244, SEQ ID No. 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEQ ID No. 317, SEQ ID No. 324, SEQ ID No. 327, SEQ ID No. 350, SEQ ID No. 363, SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID

No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID
No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID
No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID
No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID
5 No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ
ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112,
SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No.
128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID
No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ
10 ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153,
SEQ ID No. 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No.
161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID
No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ
ID No. 178, SEQ ID No. 180, SEQ ID No. 182, SEQ ID No. 184,
15 SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No.
193, SEQ ID No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID
No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ
ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219,
SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No.
20 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID
No. 242, SEQ ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ
ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262,
SEQ ID No. 264, SEQ ID No. 266, SEQ ID No. 268, SEQ ID No.
270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID
25 No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ
ID No. 289, SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295,
SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No.
303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID
No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ
30 ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330,
SEQ ID No. 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No.
338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID
No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ
ID No. 355, SEQ ID No. 357, SEQ ID No. 359, SEQ ID No. 361,
35 SEQ ID No. 364, SEQ ID No. 366, SEQ ID No. 368, SEQ ID No.
370, SEQ ID No. 372, SEQ ID No. 374, SEQ ID No. 376, SEQ ID
No. 378, SEQ ID No. 380, SEQ ID No. 382, SEQ ID No. 384, SEQ
ID No. 386, SEQ ID No. 388, SEQ ID No. 390, SEQ ID No. 392,
SEQ ID No. 394, SEQ ID No. 396, SEQ ID No. 398, SEQ ID No.

400, SEQ ID No. 402, SEQ ID No. 404, SEQ ID No. 406, SEQ ID No. 408, SEQ ID No. 410, SEQ ID No. 412, SEQ ID No. 414, SEQ ID No. 416, SEQ ID No. 418, SEQ ID No. 420, SEQ ID No. 422, SEQ ID No. 424, SEQ ID No. 426, SEQ ID No. 428 and SEQ ID No. 430.

The invention relates more particularly to a molecule of nucleic acid comprising or constituted of an encoding nucleic sequence for an olfactory receptor or for a fragment of an olfactory receptor. In the appendix, the encoding nucleic sequences for an olfactory receptor or for a fragment of an olfactory receptor are the sequences chosen among those represented in the list of sequences in the appendix under the numbers SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEQ ID No. 180, SEQ ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 193, SEQ ID No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID No. 242, SEQ ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266,

SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ ID No. 289, SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330, SEQ ID No. 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ ID No. 355, SEQ ID No. 357, SEQ ID No. 359, SEQ ID No. 361, SEQ ID No. 364, SEQ ID No. 366, SEQ ID No. 368, SEQ ID No. 370, SEQ ID No. 372, SEQ ID No. 374, SEQ ID No. 376, SEQ ID No. 378, SEQ ID No. 380, SEQ ID No. 382, SEQ ID No. 384, SEQ ID No. 386, SEQ ID No. 388, SEQ ID No. 390, SEQ ID No. 392, SEQ ID No. 394, SEQ ID No. 396, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 402, SEQ ID No. 404, SEQ ID No. 406, SEQ ID No. 408, SEQ ID No. 410, SEQ ID No. 412, SEQ ID No. 414, SEQ ID No. 416, SEQ ID No. 418, SEQ ID No. 420, SEQ ID No. 422, SEQ ID No. 424, SEQ ID No. 426, SEQ ID No. 428, SEQ ID No. 430. Evidently the invention also concerns the nucleotide sequences derived from the above sequences, for example from the degeneracy of the genetic code, and which encodes for the proteins presenting characteristics and properties of olfactory receptors. The encoding nucleic sequences for an olfactory receptor or for a fragment of an olfactory receptor are different from the pseudogenes presented in this invention. The pseudogenes correspond to the sequences in the appendix under the numbers SEQ ID No. 3, SEQ ID No. 12, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 52, SEQ ID No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID No. 60, SEQ ID No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 120, SEQ ID No. 121,

SEQ ID No. 122, SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEQ ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, 5 SEQ ID No. 233, SEQ ID No. 238, SEQ ID No. 239, SEQ ID No. 244, SEQ ID No. 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEQ ID No. 317, SEQ ID No. 324, SEQ ID No. 10 327, SEQ ID No. 350 and SEQ ID No. 363.

The invention also concerns a molecule of nucleic sequence which encode for the olfactory receptors or for fragments of olfactory receptors whose amino acid sequences are represented in the list of sequences in the 15 appendix under the numbers SEQ ID No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID 20 No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, SEQ ID No. 110, 25 SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137, SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No. 146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ ID No. 164, SEQ ID No. 30 166, SEQ ID No. 168, SEQ ID No. 170, SEQ ID No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No. 179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204, SEQ ID No. 209, SEQ ID 35 No. 211, SEQ ID No. 214, SEQ ID No. 218, SEQ ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248, SEQ ID No. 250, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 257, SEQ ID No. 263, SEQ

5 ID No. 265, SEQ ID No. 267, SEQ ID No. 269, SEQ ID No. 271,
SEQ ID No. 274, SEQ ID No. 276, SEQ ID No. 278,
SEQ ID No. 281, SEQ ID No. 284, SEQ ID No. 286, SEQ ID No.
288, SEQ ID No. 290, SEQ ID No. 294, 296, SEQ ID No. 298,
10 SEQ ID No. 300, SEQ ID No. 302, SEQ ID No. 304, SEQ ID No.
306, SEQ ID No. 308, SEQ ID No. 310, SEQ ID No. 312, SEQ ID
No. 316, SEQ ID No. 319, SEQ ID No. 321, SEQ ID No. 323, SEQ
ID No. 326, SEQ ID No. 329, SEQ ID No. 331, SEQ ID No. 333,
SEQ ID No. 335, SEQ ID No. 337, SEQ ID No. 339, SEQ ID No.
15 341, SEQ ID No. 343, SEQ ID No. 345, SEQ ID No. 347, SEQ ID
No. 349, SEQ ID No. 352, SEQ ID No. 354, SEQ ID No. 356, SEQ
ID No. 358, SEQ ID No. 360, SEQ ID No. 362, SEQ ID No. 365,
SEQ ID No. 367, SEQ ID No. 369, SEQ ID No. 371, SEQ ID No.
373, SEQ ID No. 375, SEQ ID No. 377, SEQ ID No. 379, SEQ ID
20 No. 381, SEQ ID No. 383, SEQ ID No. 385, SEQ ID No. 387, SEQ
ID No. 389, SEQ ID No. 391, SEQ ID No. 393, SEQ ID No. 395,
SEQ ID No. 397, SEQ ID No. 399, SEQ ID No. 401, SEQ ID No.
403, SEQ ID No. 405, SEQ ID No. 407, SEQ ID No. 409, SEQ ID
No. 411, SEQ ID No. 413, SEQ ID No. 415, SEQ ID No. 417, SEQ
ID No. 419, SEQ ID No. 421, SEQ ID No. 423, SEQ ID No. 425,
SEQ ID No. 427, SEQ ID No. 429 and SEQ ID No. 431.

The invention thus concerns more particularly a
purified olfactory receptor constituted by or comprising the
sequence of amino acids chosen among those represented in
25 the list of amino acid sequences under the numbers SEQ ID
No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No.
11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No.
20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No.
47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No.
30 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No.
71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No.
83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No.
92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No.
100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID
35 No. 108, SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ
ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137,
SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No.
146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID
No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ

5 ID No. 164, SEQ ID No. 166, SEQ ID No. 168, SEQ ID No. 170,
SEQ ID No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No.
179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID
10 No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ
ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204,
SEQ ID No. 209, SEQ ID No. 211, SEQ ID No. 214, SEQ ID No.
218, SEQ ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID
No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ
15 ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248,
SEQ ID No. 250, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No.
257, SEQ ID No. 263, SEQ ID No. 265, SEQ ID No. 267, SEQ ID
No. 269, SEQ ID No. 271, SEQ ID No. 274, SEQ ID No. 276, SEQ
ID No. 278, SEQ ID No. 281, SEQ ID No. 284, SEQ
20 ID No. 286, SEQ ID No. 288, SEQ ID No. 290, SEQ ID No. 294,
296, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 302, SEQ ID
No. 304, SEQ ID No. 306, SEQ ID No. 308, SEQ ID No. 310, SEQ
ID No. 312, SEQ ID No. 316, SEQ ID No. 319, SEQ ID No. 321,
SEQ ID No. 323, SEQ ID No. 326, SEQ ID No. 329, SEQ ID No.
331, SEQ ID No. 333, SEQ ID No. 335, SEQ ID No. 337, SEQ ID
25 No. 339, SEQ ID No. 341, SEQ ID No. 343, SEQ ID No. 345, SEQ
ID No. 347, SEQ ID No. 349, SEQ ID No. 352, SEQ ID No. 354,
SEQ ID No. 356, SEQ ID No. 358, SEQ ID No. 360, SEQ ID No.
362, SEQ ID No. 365, SEQ ID No. 367, SEQ ID No. 369, SEQ ID
No. 371, SEQ ID No. 373, SEQ ID No. 375, SEQ ID No. 377, SEQ
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SEQ ID No. 387, SEQ ID No. 389, SEQ ID No. 391, SEQ ID No.
393, SEQ ID No. 395, SEQ ID No. 397, SEQ ID No. 399, SEQ ID
No. 401, SEQ ID No. 403, SEQ ID No. 405, SEQ ID No. 407, SEQ
ID No. 409, SEQ ID No. 411, SEQ ID No. 413, SEQ ID No. 415,
SEQ ID No. 417, SEQ ID No. 419, SEQ ID No. 421, SEQ ID No.
423, SEQ ID No. 425, SEQ ID No. 427, SEQ ID No. 429 and SEQ
ID No. 431.

35 Another aim of the invention is polyclonal or
monoclonal antibodies directed against at least one receptor
of the invention, a derivative or a fragment of these. These
antibodies can be prepared by the methods described in the
literature. According to prior art techniques, polyclonal
antibodies are formed by the injection of proteins,
extracted from the epithelium or produced by genetic

transformation of a host, into animals, and then
recuperation of antiserums and antibodies from the
antiserums for example by affinity chromatography. The
monoclonal antibodies can be produced by fusing myeloma
5 cells with spleen cells from animals previously immunised
using the receptors of the invention. These antibodies are
useful in the search for new olfactory receptors or the
homologues of these receptors in other mammals or again for
studying the relationship between the receptors of different
10 individuals or species.

The invention also concerns a vector comprising
at least one molecule of nucleic acid above, advantageously
associated with adapted control sequences, together with a
production or expression process in a cellular host of a
15 receptor of the invention or a fragment thereof. The
preparation of these vectors as well as the production or
expression in a protein host of the invention can be carried
out by molecular biology and genetic engineering techniques
well known to the professional.

20 A molecule of encoding nucleic acid for an
olfactory receptor or a vector according to the invention
can also be used to transform animals and establish a line
of transgenic animals.

25 The vector used is chosen in function of the
host into which it is to be transferred; it can be any
vector such as a plasmid.

Thus the invention also relates to cellular
hosts expressing olfactory receptors obtained in conformity
30 with the preceding processes.

The invention also relates to nucleic and
oligonucleotide probes prepared from the molecules of
nucleic acid according to the invention.

35 These probes, marked advantageously, are useful
for hybridisation detection of similar receptor sequences in
other individuals or species. According to prior art
techniques, these probes are put into contact with a
biological sample. Different hybridisation techniques can be

used, such as Dot-blot hybridisation or replica hybridisation (Southern technique) or other techniques (DNA chips). Such probes constitute the tools making it possible to detect similar sequences quickly in the encoding genes for olfactory receptors which allow study of the presence, origin and preservation of these proteins.

The oligonucleotides are useful for PCR experiments, for example to search for genes in other species or with a diagnostic aim.

The olfactory receptors are proteins with 7 transmembranous domains coupled with G proteins. Attachment of a ligand to a receptor brings about a change in the conformation of the receptor, and inside the cell, and this signal is transduced through the intermediary of second messengers. Consequently, the aim of the invention is a screening process for compounds capable of constituting ligands of the receptors described above consisting of putting in contact one compound and one or several of said receptors and of measuring by any appropriate means the affinity between said compound and said receptor.

The contact between the compound to be tested and the olfactory receptor or receptors of the invention can be carried out by using the hosts described above and expressing said receptors at least at their surface. It can consist of a line of immortalised cells, olfactory or not, transfected by a vector carrying cDNA making it possible to express at its surface and at a high level a functional recombinant olfactory receptor. If the compound tested constitutes a ligand, its contact with the transformed cells, induces intracellular signals which result from the fixation of said compound on the receptor.

The contact of the compounds to be tested with the receptors of the invention can also be carried out by fixing one or several receptors on one or several membranes. The olfactory receptors of the invention can thus also be integrated with a bio-sensor. In such a system, it is possible to visualise in real time the interactions between the compound being tested and the receptor. One of the

partners of the couple receptor/ligand is fixed on an interface which can contain a matrix covered with aliphatic chains. This hydrophobic matrix can easily be covered with a lipidic layer by spontaneous fusion of liposomes injected into its contact. Olfactory receptors inserted in the liposomes or vesicles can thus be integrated into the biosensors. The ligands are thus analysed with regard to one or several different olfactory receptors.

The above methods make it possible to determine whether a compound activates or inhibits the receptors. In this embodiment, it is advantageous to use a known ligand which allows measurement by competition.

The invention also relates to a compound as yet unknown constituting a ligand of an olfactory receptor, identified and selected by the above process.

The receptors of the invention find applications in very varied domains such as:

- the food processing industry, for detection of aromas, quality control, analysis of samples.
- perfumery, for the analysis or comparison of perfumes,
- the environment, for detecting toxic substances, such as gases or for trapping odours.

The sequence data from this invention have been deposited with the DDBJ/EMBL/GenBank Data Libraries under accession numbers AF022649, AF073959-073989, AF127814-127907, and AF179716-179846.

Other advantages and characteristics of the invention will become apparent by reading the following examples concerning the identification and cloning of olfactory receptor genes and pseudogenes of mouse and primates, and which refer to the attached drawings in which:

- Figure 1 represents a schematic phylogeny tree of the primate species used in the present study and adapted from (32).
- Figure 2 represents a comparison of the deduced protein OR sequences obtained from the different

primate species characterized in this study. The dendrogram was established using the PileUp program from the GCG Package. Percent ASI was determined by pairwise sequence comparisons using the Gap program and is indicated along the abscissa of the tree. Sequences from the literature are indicated by an asterisk. Human OR sequences derived from the use of the OR3B/OR5B primers and representing the main OR families were selected from (3, 13). Dog (CfOLF1 and its human counterpart HsOLF1; CfOLF2) and chicken (COR4) sequences were selected from (4) and (7) respectively. OR families (greater than 40% ASI) are indicated by open circles and subfamilies (greater than 60% ASI) by open squares. The main family was arbitrarily named family 1 and subdivided in 2 groups of subfamilies, 1-I and 1-II (ovals). Group 1-II comprises subfamilies A and B. Beside the sequence names, black dots indicate sequences derived from the use of the OR3B/OR5B consensus primers, black squares those derived from the OR3.1/7.1 consensus primers, and black rectangles indicate potentially functional genes (uninterrupted ORFs). In the case of HSA 912-93 (black rectangle and double asterisk), this sequence contains only one non-sense point mutation in human, but is potentially coding in other primates (13). Human, HSA; chimpanzee, PTR; gorilla, GGO; orangutan, PPY; gibbon, HLA; macaque, MSY; baboon, PPA; marmoset, CJA; squirrel-monkey, SSC and SBO; lemur, EFU and ERU; zebrafish, DRE (see Table 1).

- Table 1 represents an estimation of the fraction of pseudogenes in the OR gene repertoire of primate species and mouse. OR sequences were established by sequencing PCR products generated using consensus OR primers OR3B/OR5B and OR3.1/OR7.1 on genomic DNA. Data for human are derived from Rouquier et al. (3) and this study. The 3 zebrafish sequences characterized in this work are indicated. The average pseudogene percentage for each branch was estimated by summing the percentage of each species divided by the number of species.

I. Materials and Methods.

I.1. Cloning and analysis of OR-like sequences in primates and mouse.

The isolation of OR-related sequences has been described elsewhere (3, 13). Briefly, 100 ng of genomic DNA from each species was subjected to PCR using consensus OR primers OR5B-OR3B (OR5B (TM2), 5'-CCCATGTA(T/C)TT(G/C/T)TT(C/T)CTC(A/G/T)(G/C)(C/T)AA(C/T)(T/C)T(G/A)TC-3' ; PMY(F/L)FL(S/A/T/G/C)NLS ; OR3B (TM7), 5'-AG(A/G)C(A/T)(A/G)TAIATGAAIGG(A/G)TTCAICAT-3' ; M(L/F/V/I)NPF(I/M)Y(S/C)L) (14). A second pair of consensus primers, OR3.1-OR7.1 (OR3.1 (TM3), 5'-GCIATGGCITA(C/T)GA(C/T)(A/C)GITA-3' ; AMAYD(S/R)Y ; OR7.1 (TM7), 5'-A(A/G)I(G/C)(A/T)(A/G)TA(A/G/T)AT(A/G)AAIGG(A/G)TT-3' ; NPFIIY(S/R/T/C/W)(L/F)) (15, 16), was also used to amplify primate OR sequences. PCR products were subcloned in the TA vector (InVitrogen), and recombinant clones were identified by PCR. Sequencing of the OR sequences was performed and sequences were assembled and analyzed as detailed elsewhere (3). The following species were studied: human (*Homo sapiens*, HSA), chimpanzee (*Pan troglodytes*, PTR), gorilla (*Gorilla gorilla*, GGO), orangutan (*Pongo pygmaeus*, PPY), gibbon (*Hylobates lar*, HLA), macaque (*Macaca sylvanus*, MSY), baboon (*Papio papio*, PPA), marmoset (*Callithrix jacchus*, CJA), squirrel-monkey (*Saimiri sciureus*, SSC, and *Saimiri boliviensis*, SBO), lemur (*Eulemur fulvus*, EFU, and *Eulemur rubriventer*, ERU), and mouse (*Mus musculus domesticus*, MMU). In addition, a few zebrafish (*Danio rerio*, DRE) sequences were characterized using primers OR3.1-OR7.1.

Pairwise sequence comparisons and multiple alignments were performed using Gap and PileUp from the GCG package (Wisconsin Package version 8).

I.2. Construction and screening of an OR-specific mouse sublibrary.

Mouse OR clones obtained by PCR as described above were gridded in 96-well microtiter dishes (1536 clones in 8 plates). For hybridization screening, the clones were

robot-spotted in duplicate on high-density filters as described elsewhere (17). Approximately 90% of the clones were identified as OR genes. This library was screened to identify clones hybridizing to human OR pseudogene sequences. Human plasmid DNA probes were radiolabeled to a specific activity of 10^8 - 10^9 cpm/ μ g by random hexamer priming (18) using (γ - 32 P)-dCTP (Amersham). Filter hybridizations were carried out under standard hybridization conditions (19), and exposed to Kodak X-ray film at -80°C . Three human OR probes were used: OR1-72, OR912-47, OR15-71 (DDBJ/GenBank accession numbers U86218, U86230, U86296 respectively).

II. Results.

II.1. Isolation and analysis of primate OR sequences.

To sample the OR genes in primate species, OR genes from anthropoids and prosimians were randomly sequenced (Fig. 1). OR genes were obtained by PCR on genomic DNA from the different species using consensus OR primer pairs OR5B-OR3B and OR3.1-OR7.1 chosen respectively in the transmembrane domains TM2 and TM7, and TM3 and TM7. Except human, eighteen to thirty-five individual OR clones were sequenced per taxon. A total of 221 OR sequences, representing 10 species, was analyzed. These sequences are distributed in different groups whose percentage of nucleotide sequence identity (NSI) ranges from ~35 to >99% (not shown). The corresponding amino-acid sequences were compared to a variety of OR sequences from the public databases and previous studies (3). All sequences have the characteristic features of olfactory receptors, with a heptahelical structure and conserved motifs as previously defined (1, 3, 14). The use of two pairs of consensus primers made our sampling representative of the OR gene repertoire. Primate sequences are distributed in 7 families (sequences that share >40% amino-acid identity (ASI) define a family), and 56 subfamilies (ASI>60%), with group 1-II of family 1 representing the zone of overlap of sequences

derived from using the two primer pairs (Fig. 2). Non-human primate OR genes are represented in 6 families and about 45 subfamilies. Numerous sequences are grouped in family 1 (~66%) comprising subfamily 1A, the largest subfamily (57/221, 26%). Subfamily 1B is almost devoid of coding human OR sequences (Fig. 2). Subfamily 1A contains only human pseudogenes originating from chromosomes 14 and 19 (not shown) whereas subfamily 1B contains human pseudogenes lying on various chromosomes (not shown) (3). As the Applicant found previously for human (3), the amino-acid sequences deduced from the non-human primate sequences revealed many pseudogenes (Fig. 2 and Table 1). Table 1 provides information about the evolution of the pseudogene fraction along with the evolution of primates. Hominoids present the highest fraction of pseudogenes (39 to >70%, average ~50%). Old world monkeys (macaque and baboon) have a lower pseudogene fraction (20 to 35%, average 27%), while even fewer pseudogenes were found among the sequences derived from new world monkeys. Only one pseudogene (SB064) was identified among the 49 sequences obtained from marmoset and two species of squirrel-monkey. In contrast, 37% of the prosimian lemur OR sequences were pseudogenes.

II.2. Sequence analysis of mouse OR sequences.

To test whether mammals thought to be microsmatic or macrosmatic differ in the fraction of pseudogenes in their OR repertoire, OR sequences in the mouse genome were surveyed. A mouse sublibrary enriched for OR-related sequences amplified by PCR from the mouse genome was constructed (see materials and methods).

Nineteen randomly selected mouse OR clones were sequenced. All 19 have an uninterrupted open-reading frame (ORF) and are potentially functional. These sequences group primarily in family 1 (not shown) and vary from ~52 to >99% NSI (not shown). In addition, in an attempt to bias in favor of selecting mouse OR pseudogenes, the Applicant searched for mouse OR sequences homologous to human pseudogenes. One member was chosen from three different OR pseudogene families: clones 1-72, 15-71 and 912-47 from chromosomes 1,

15 and 11, respectively (3). Each of these genes belongs to one of the 3 main groups of human OR sequences and has accumulated a number of mutations such as stop codons and indel frameshifts (3). The amino-acid sequence identity
5 between these three ranges from 31% to 41%.

High density filters from the mouse OR sublibrary were then hybridized separately with the three human pseudogene probes at a high stringency. Fourteen clones were sequenced on both strands. These sequences
10 showed 38% to 53% ASI to the human sequences used to select them, indicating that they are not the orthologs of the human pseudogenes. All have an uninterrupted ORF from TM2 to TM7 (not shown). Together, 33 mouse OR sequences were sequenced, none of which containing characteristic features
15 of pseudogenes.

III. Discussion.

What is the basis for the differences in olfactory ability observed among mammals? Diverse reasons
20 have been suggested that could account for these differences, i.e. the size of the anatomical structures devoted to olfaction (olfactory epithelium, olfactory bulb, cortical structures), or the number of OR families/subfamilies, and the total number and diversity of
25 expressed OR genes. The olfactory epithelial surface of macrosmatic animals such as dogs is larger than in microsmatic humans ((4) and references therein). On the other hand, using unique dog sequence probes that represent specific OR subfamilies and which will not cross-hybridize
30 with other subfamilies, comparative analyses have been performed by Southern blot analysis among a panel of mammals including dog and human. This study indicates that the number of OR sequences per subfamily is similar in microsmatic and macrosmatic animals (4). Recently the
35 Applicant demonstrated that a high fraction (>70%) of the human OR genes have been mutated during evolution into pseudogenes (3). The Applicant found that chromosomes 7, 16 or 17 contained a high fraction of potentially coding OR sequences, whereas other chromosomes such as chromosome 3

(3, 20) or 11 (3) contained primarily pseudogenes. Other studies on chromosome 17 (14, 21), and on chromosome 11 (22) in which 75% of the OR sequences identified were pseudogenes, support these observations. These findings led us to hypothesize that the number of functional OR genes could be correlated to the olfactory capability of a given animal. In an attempt to test this hypothesis, the OR gene repertoire of the main primate species, thought to be microsmatic, and of mouse, thought to be macrosmatic were sampled. The Applicant's analysis clearly indicates that (see Fig. 1 and Table 1) from new world monkeys to hominoids, there is an increase during evolution of the percentage of OR pseudogenes from ~0 to ~70%, with the highest pseudogene content observed in gorilla, chimpanzee and human. Supporting this observation, during the course of this work, Sharon and colleagues (23) published a study about the evolution in primates of the OR genes orthologous to the human OR gene cluster located on chromosome 17p13.3 (14, 21). The authors conclude to a rapid decline (~10 Mya, corresponding to the radiation of hominoids) of the functional OR repertoire in mammals. In addition, the Applicant showed in a recent study that this pool of pseudogenes is still growing in human, which will probably evolve towards a minimal set of functional OR genes (13). It is therefore likely that there is a selective advantage for new world monkeys to retain a high proportion of functional OR genes whereas this advantage appears to be reduced in old world monkeys. The prosimian branch represented by two lemur species does not follow this rule and has accumulated a high fraction of OR pseudogenes (Table 1). This particular taxon is localized in Madagascar and is composed of diurnal (as *Eulemur fulvus*) and nocturnal (as *Eulemur rubriventer*) animals, both of which are thought to have evolved from a common ancestral species. The two species showed no striking difference in the OR pseudogene fraction suggesting that loss of functional OR genes preceded their divergence. Nevertheless, despite the number of OR families and subfamilies presented in this study (Fig. 2), the collection of sequences of the present work represents a subset of OR

genes and it is still possible that the fraction of functional OR genes and OR pseudogenes could be reversed in other segments of the OR family in different species. However, although some studies indicate that mouse or dog display better olfactory performances than human (10, 24), accurate experiments to compare the olfactory ability between the different primates species remain to be conducted to support our hypothesis.

All OR sequences the Applicant derived from mouse are potentially coding. No pseudogenes were detected either by sequencing randomly selected OR sequences or by deliberately screening with human OR pseudogene probes. This indicates that the OR pseudogene content is either zero or restricted to rare examples in mouse (25).

Taken together, this study led us to hypothesize that the reduction of the sense of smell could correlate with the fraction of functional OR genes in the genome. This observation would probably result from the relaxation of the selective pressure exerted on the different species, i.e. as soon as the function becomes non-essential for the survival or the social behavior of a particular species, the genes responsible for that function tend to accumulate deleterious mutations. Actually, it is likely that the different hypotheses evoked to explain the loss of function would be not exclusive, but that a parallel might exist between the reduction of the anatomical structures devoted to olfaction, the decrease in the number of functional OR genes, and the reduction of the sense of smell. This hypothesis is strongly supported by the fact that aquatic mammals such as dolphin which has a reduced olfactory apparatus, have only OR pseudogenes (15). These animals live in water and do not need to smell volatile odorants. Therefore, a parallel degeneration of the olfactory organs and the OR gene repertoire has occurred probably due to the relaxation of the selective constraints. This sort of observation has also been made in the blind marsupial mole, in which degeneration of the eyes is accompanied by mutation of the interphotoreceptor retinoid binding protein gene, which is

involved in the regeneration of rhodopsin in the visual cycle (26).

However, it is difficult to measure and compare the olfactory efficiency of different animal species. Various parameters such as the threshold of detection of odorants (sensitivity), the range of odors detectable and the discriminatory power (acuity) are key parts of the olfactory ability. Thus it is uncertain to determine precisely which of these parameters are taken in account when comparing two species, and therefore the origin of the olfactory deficiency of primates remains a controversial and difficult point to address. Furthermore, there is no data available in the literature comparing the olfactory ability between the different primate species studied in this work, and most of the few studies conducted to compare the performances of mouse or dog versus human concern either the threshold of detection of very few odorants (for example the n-amyl acetate (27)) or the observation that trained dogs are far better than human to detect hidden objects such as mines, drugs, or scavenged people after natural disasters (28, 29). None the less, if the fraction of OR pseudogenes has been estimated in mouse, it remains to be determined in dog.

The chromosomal distribution of the OR gene repertoire arose through multiple duplication rounds (3, 5, 20, 30, 31) giving rise to paralogous regions. Even though the number of duplication events may be different among the mammals, overall it appears that the number of OR genes was established before the divergence of mammals (4). This explains why by Southern analysis there is no striking difference in the number of OR genes of four different subfamilies between the sea lion, which has an underdeveloped olfactory apparatus, and other mammals (4). On the other hand, the Southern blot approach does not reveal the functionality of the OR sequences, and the Applicant predicts that a large fraction of the sea lion OR genes could be pseudogenes as has been described for the dolphin (23). Similarly striking differences have been observed in the olfactory ability of different breeds of

dogs (12). Despite the variations in the size of the olfactory epithelium of the different breeds ((12) and references therein), it would be interesting to know what the biological basis is for the differences in performances observed between sight and scent hounds. One obvious possibility is loss of functional OR genes, but, given the recent origin of all modern dogs this explanation seems unlikely. Other explanations could be changes in behavior, or in expression brought about by the modification of a key master transcription factor or in the unusual mechanism that allows only one OR gene allele or the other to be expressed exclusively in any one epithelium cell.

Finally, the Applicant hypothesizes that the study of the evolution of the olfactory receptor gene repertoire through the determination of the pseudogene fraction, could mirror the evolution of the olfactory sensory function in micro- and macrosmatic mammals.

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Species						
	Common name		Number of sequences analyzed	% ORF	% pseudogenes	Average % pseudogenes
Hominoids	Human	Homo sapiens (HSA)	99	30	70	50 %
	Chimpanzee	Pan troglodytes (PTR)	21	52	48	
	Gorilla	Gorilla gorilla (GGO)	18	50	50	
	Orangutan	Pongo pygmaeus (PPY)	23	61	39	
	Gibbon	Hylobates lar (HLA)	22	59	41	
Old world monkeys	Macaque	Macaca sylvanus (MSY)	20	65	35	27 %
	Baboon	Papio papio (PPA)	21	81	19	
New world monkeys	Marmoset	Callithrix jacchus (CJA)	19	100	0	2 %
	Squirrel-monkey	Saimiri sciureus (SSC)	15	100	0	
		Saimiri boliviensis (SBO)	15	93	7	
Prosimians	Lemur	Eulemur fulvus (EFU)	19	58	42	37 %
		Eulemur rubriventer (ERU)	16	69	31	
Rodents	Mouse	Mus musculus (MMU)	33	100	0	0 %
Fish	Zebrafish	Danio rerio (DRE)	3	100	0	0 %

Table 1

CLAIMS

1. Molecule of nucleic acid constituted by or comprising a sequence chosen among those represented in the list of sequences in the appendix under the numbers SEQ ID

5 No. 3, SEQ ID No. 12, SEQ ID No. 21, SEQ ID No. 22, SEQ ID No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 52, SEQ ID

10 No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID No. 60, SEQ ID No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 120, SEQ ID No. 121, SEQ ID No. 122,

15 SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEQ ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 233, SEQ ID No. 238, SEQ ID No. 239, SEQ ID No. 244, SEQ ID No.

20 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEQ ID No. 317, SEQ ID No. 324, SEQ ID No. 327, SEQ ID No. 350, SEQ ID No. 363, SEQ ID No. 1, SEQ ID No. 4, SEQ ID No.

25 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No.

30 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ

35 ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 155, SEQ ID No. 157, SEQ

5 ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165,
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ID No. 428 and SEQ ID No. 430.

35 2. Molecule of nucleic acid according to claim
1, wherein said sequence is an encoding nucleic sequence for
an olfactory receptor or for a fragment of an olfactory
receptor and is chosen among those represented in the list

of sequences in the appendix under the numbers SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEQ ID No. 180, SEQ ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 193, SEQ ID No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID No. 242, SEQ ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266, SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ ID No. 289, SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330, SEQ ID No. 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ ID No. 355,

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3. Molecule of encoding nucleic sequence for the olfactory receptors or for fragments of olfactory receptors whose amino acid sequences are represented in the list of sequences in the appendix under the numbers SEQ ID No. 2, 15 SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ 20 ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, 25 SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137, SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No. 146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ ID No. 30 164, SEQ ID No. 166, SEQ ID No. 168, SEQ ID No. 170, SEQ ID No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No. 179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204, SEQ ID No. 35 No. 209, SEQ ID No. 211, SEQ ID No. 214, SEQ ID No. 218, SEQ ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248, SEQ ID

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4. A purified olfactory receptor constituted by or comprising the sequence of amino acids chosen among those represented in the list of amino acid sequences under the numbers SEQ ID No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135,

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5. A polyclonal or monoclonal antibody directed against at least one receptor according to claim 4 or a derivative or a fragment thereof.

5 6. A vector comprising at least one molecule of nucleic acid according to one or the other of Claims 1 or 3, advantageously associated with control sequences.

10 7. Production process of a receptor according to claim 4, comprising the following steps:

- transferring a molecule of nucleic acid according to one or the other of claims 2 or 3 or a vector according to Claim 6 into a host,
- 15 - cultivating said cellular host in conditions allowing production of the protein constituting the receptor,
- isolating said proteins, by all appropriate means.

20 8. Expression process of a receptor according to claim 4 in a host, comprising the following steps:

- transferring a molecule of nucleic acid according to one or the other of claims 2 or 3 or a vector according to Claim 6 into a host,
- 25 - cultivating said host in conditions allowing expression of said receptors at the surface of the host.

30 9. A host transformed by a molecule of nucleic acid according to one or other of claims 2 or 3 or by a vector according to Claim 6.

35 10. Screening procedure of compounds capable of constituting ligands of a receptor according to claim 4, wherein the said compounds are put into contact one or several of said receptors then the affinity between said compound and said receptor is measured by all appropriate means.

11. A membrane on which one or several receptors are fixed according to claim 4 useful for applying a process according to claim 10.

5 12. A compound constituting a ligand of an olfactory receptor, identified and selected by the process according to claim 10.

10 13. Utilisation of a receptor according to claim 4, of a host according to claim 9 or of a membrane according to claim 11, for the detection of aromas, quality control, sample analysis, analysis or comparison of perfumes, detection of toxic substances, or the trapping

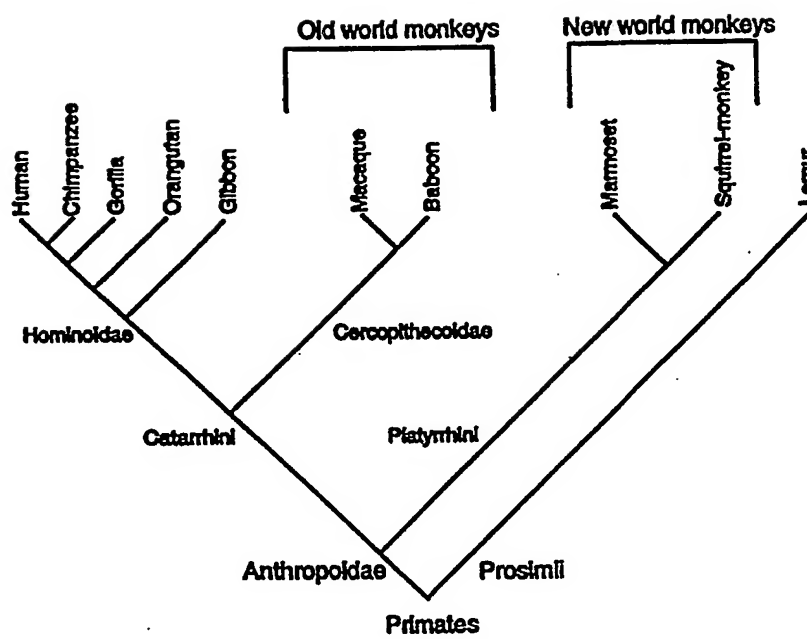


Figure 1

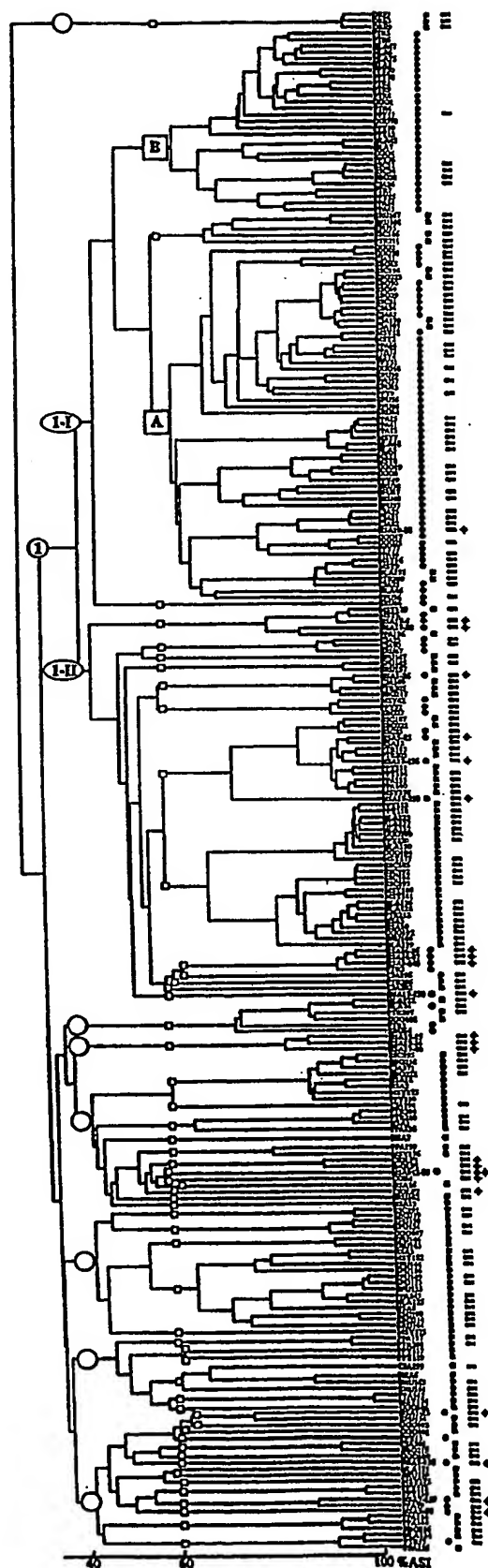


FIGURE 2

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Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
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85

90

95

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 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160

atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529
 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175

cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
 180 185 190

ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg 625
 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
 195 200 205

gtg atg tac acg gtg gtt acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 5

<211> 216

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA15; Accession DDBJ/EMBL/GenBank = AF127816

<400> 5

Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 6
<211> 649
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9557; gene = PPA; Accession DDBJ/EMBL/GenBank = AF27817
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 6

c tgg gtt gac atc tgt ttc agc acc tgc atc gtc ccc aag atg ctg gtg	49
Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys Met Leu Val	
1 5 10 15	
aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc	97
Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr	
20 25 30	
cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg	145
Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu	
35 40 45	
acc gtg atg gcc tat gac cgg ttt gtg gcc atc tat cac tcc ctg cac	193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His	
50 55 60	
tac acg gtc atc atg agc ccc cgg ctc tgt gga ctg ctg gtt ctg gga	241
Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly	
65 70 75 80	
tcc tgg tgc atc agt gtc atg ggt tcc ctg ctt gag acc ttg act gtt	289
Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val	
85 90 95	
ttg agg ctg tcc ttc tgc atc aaa atg gaa att cca cac ttt ttt tgt	337
Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys	
100 105 110	
gat ctt cct gaa gtc ctg aag ctc gcc tgt tct gac acc ttc atc aat	385
Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn	
115 120 125	
aat gta gtg ata tac ttt gca act ggc att ctg gct gtg att ccc ttt	433
Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe	
130 135 140	
act gga ata ctt ttc tct tac tat aaa att gtt ttc tct gta ctg agg	481
Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg	
145 150 155 160	
att tcc tca gct ggg gga aag tac aaa gcc ttt tcc acc tgt ggt tcc	529
Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser	
165 170 175	
cac ctc tca atg gtc agc ttg ttc tat ggc acg ggc ctt ggg gtc tat	577
His Leu Ser Met Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr	
180 185 190	
ctc agt tct gca gct ata cca tct tct agg aca agt ctg gtg gcc tca	625
Leu Ser Ser Ala Ala Ile Pro Ser Ser Arg Thr Ser Leu Val Ala Ser	
195 200 205	
gtg atg tac acc atg gtc acc ccc	649
Val Met Tyr Thr Met Val Thr Pro	

210

215

<210> 7
<211> 216
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9557; gene = PPA; Accession DDBJ/EMBL/GenBank = AF27817
<400> 7

Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His
50 55 60

Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
65 70 75 80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
85 90 95

Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
115 120 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe
130 135 140

Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg
145 150 155 160

Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Met Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Ile Pro Ser Ser Arg Thr Ser Leu Val Ala Ser
 195 200 205

Val Met Tyr Thr Met Val Thr Pro
 210 215

<210> 8
 <211> 649
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9557; gene = PPA41; Accession DDBJ/EMBL/GenBank = AF127818
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 8
 c tgg gtt gac atc tgt ttc agc acc tgc atc gtc ccc aag atg ctg gtg 49
 Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc 97
 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30
 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg 145
 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45
 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60
 tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc 241
 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
 65 70 75 80
 acg tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg 289
 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
 85 90 95
 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337
 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385
 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125
 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc 433
 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
 130 135 140
 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag 481
 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160
 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529
 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175
 cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
 180 185 190
 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg 625
 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
 195 200 205
 gtg atg tac acg gtg gtt acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 9

<211> 216

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA41; Accession DDBJ/EMBL/GenBank = AF127818

<400> 9

Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 10

<211> 649

<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA42; Accession DDBJ/EMBL/GenBank = AF127819

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 10

210

215

<210> 11
<211> 216
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9557; gene = PPA42; Accession DDBJ/EMBL/GenBank = AF127819
<400> 11
Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys Met Leu Val
1 5 10 15

Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
35 40 45

Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
65 70 75 80

Pro Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
85 90 95

Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys
100 105 110

Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
115 120 125

Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
130 135 140

Ile Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Ala Ala Ile Met Lys
145 150 155 160

Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
 180 185 190

Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala
 195 200 205

Val Met Tyr Thr Ala Val Thr Pro
 210 215

<210> 12
 <211> 641
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(641)
 <223> Taxon = 9557; gene = PPA43; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF127820
 <400> 12
 cttgcctgac atcagtttca ccttggccat ggtccccaag atgattgtgg acatgcaatc 60
 gcatagcaga gtcattctccc acgcggactg cctggcacag atgtctttct ttgtcctttt 120
 tgcattgata gatgacatgc tcctgactgt gatggcctat aactgatttg tggccatctg 180
 tcaccccttg cactaccag tcattcatgaa tctcacttc tgtgtcttct tagtttttgt 240
 gtctttttcg tcagcgtggt ggattcccag ctgcacaatt tgattgtggt acaacttacc 300
 tgcttcaatg atgtggaaat ctctaaattt ttctgtgacc cttctcaact tctcaatcct 360
 agcctgctct gacacataac atagtcgtat attttattgg taccatattt ggttttcttc 420
 ctctctcagg gatccttttc ttttactata aaattgtttc ctccattccg agagtctgct 480
 cttcaggtag gaagtataaa gcctttctcca cctgcagctc tcacctttca gttgttttgt 540
 tattttatgg aacagccctt ggagggtacc tcagttcagc tgtctctctc cccccagga 600
 aggggtgcagc ggcctcagtg atgtacatgg tggtcacccc c 641

<210> 13
 <211> 649
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(649)

<223> Taxon = 9557; gene = PPA68; Accession DDBJ/EMBL/GenBank = AF127821

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 13

c ttc ata gac gtc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg 49
Phe Ile Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aac atc cag aca cag agc aga gtc atc acc tat gca ggc tgc atc acc 97
Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
20 25 30

cag atg tgc ttt ttc ata ttc ttt gcg gga ctg gat atc ttt atg ctg 145
Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
35 40 45

acc gtg atg gcc tat gac agg ttt gtg gcc atc tgt cac ccc ctg cac 193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac acg gtc acc atg aac ccc agg ctc tgt gga ctg ctg gtt ctg gcg 241
Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

tcc tgg atc atg agt gcc ctg aat tct tcg ttg caa agc tta atg gta 289
Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val
85 90 95

ttg cac ctt tcc ttc tgt gca gac ttg gaa att ccc cac ttt ttc tgt 337
Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

gaa ctt aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat 385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

gac atg gtg atg tat ttg gca tct gcg ctg ctg ggc ggt ggt gcc ctc 433
Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
130 135 140

tct ggg atc ctt tat tct tat tct aag atc gtt tcc tcc ata cgt gga 481
Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
145 150 155 160

acc tcg tca gct cag ggg aag tac aag gca ttt tcc acc tgt gca tct 529
Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

cac ctc tcg gtt gtc tcc tta ttt tat ggt acg ctc cta gga gtg tac 577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
180 185 190

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
 145 150 155 160

Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 15

<211> 649

<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA72; Accession DDBJ/EMBL/GenBank = AF127822

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 15

c ttc ata gac atc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg 49

Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val

1

5

10

15

aac atc cag aca cag agc aga gtc atc acc tat gca ggc tgc atc acc 97

Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr

20

25

30

cag atg tgc ttt ttc ata ttc ttt gcg gga ctg gat atc ttt atg ctg 145

Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu

35

40

45

acc gtg atg gcc ttt gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193

Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His

50

55

60

tac acg gtc acc atg aac ccc aag ctc tgt ggg ctg ctg gtt ctg gcg 241

Tyr Thr Val Thr Met Asn Pro Lys Leu Cys Gly Leu Leu Val Leu Ala

65

70

75

80

tcc tgg atc atg aat gcc ctg aat tcc tcg tta caa agc tta ata gtg 289

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Ser Trp Ile Met Asn Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
      85                      90                      95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa att ccc cac ttt ttc tgt      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
      100                      105                      110

gaa ctt aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat      385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
      115                      120                      125

gac atg ggg atg tat atg gca tct gct ctg ctg ggc ggt ggt gcc ctc      433
Asp Met Gly Met Tyr Met Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
      130                      135                      140

tct ggg atc ctt tat tct tat tct aag atc ctt tcc tcc ata cgt gga      481
Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Leu Ser Ser Ile Arg Gly
      145                      150                      155                      160

acc tcg tca gct cag ggg aag tac aag gca ttt tcc acc tgt gca tct      529
Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165                      170                      175

cac ctc tcg gtt gtc tct tta ttt tat ggt acg ctc cta gga gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
      180                      185                      190

ttt agt tct gct gca act cgt aac tca cac tca agt gct gca gcc tcg      625
Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
      195                      200                      205

gtg atg tac acg gtg gtt acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
      210                      215

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<210> 16

<211> 216

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA72; Accession DDBJ/EMBL/GenBank = AF127822

<400> 16

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Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1              5              10              15

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Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
      20              25              30

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Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu

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[illegible]

<223> Taxon = 9557; gene = PPA79; Accession DDBJ/EMBL/GenBank = AF127823

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 17

c ctt gtc gat gtc tcc tat gcc aca agc ata gtc cct cag ctg ctg gca 49
Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala
1 5 10 15

cat ttt ctt gca gaa cat aaa gcc atc tcg ttg cag agc tgt gca gcc 97
His Phe Leu Ala Glu His Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala
20 25 30

caa tta ttt ttc tcc ctg gcc ttg ggt ggg att gag ttt gtt ctc ctg 145
Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
35 40 45

gca gtg atg gcc tat gac cgc tat gtg gct gtg tgt gac ccc ctg cga 193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg
50 55 60

tac tca gcc acc atg cat gga gcg cta tgt gct aag ttg gcc atc aca 241
Tyr Ser Ala Thr Met His Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr
65 70 75 80

tcc tgg gtc agt gga tcc att aac tct ctc atg cat acc acc atc acc 289
Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Met His Thr Thr Ile Thr
85 90 95

ttt cag ctg ccc atg tgc aca aac aag ttt att aat cat ata ttc tgt 337
Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asn His Ile Phe Cys
100 105 110

gaa att cta gct gtg atc agg ctg gct tgt gtg gac acc tcc tcc aac 385
Glu Ile Leu Ala Val Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn
115 120 125

gag gtc acc atc atg gtg tct agc att gtt ctt ctg atg aca ccc tta 433
Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Leu
130 135 140

tgt ctg gtt ctt ttg tct tac atc cgg atc atc tcc acc atc tta aag 481
Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys
145 150 155 160

atc cag tcc aga gaa gga agg agg aaa gcc ttc cac acg tgt gcc tct 529
Ile Gln Ser Arg Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser
165 170 175

cac ctc aca gtg gtt gcc ctg tgc tat ggc atg gcc att ttc act tac 577
His Leu Thr Val Val Ala Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr
180 185 190

Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Leu
130 135 140

Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys
 145 150 155 160

Ile Gln Ser Arg Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser
 165 170 175

His Leu Thr Val Val Ala Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr
 180 185 190

Ile His Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser
 195 200 205

Leu Phe Tyr Ala Ile Leu Thr Pro
 210 215

<210> 19
 <211> 649
 <212> DNA
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9598; gene = PTR12; Accession DDBJ/EMBL/GenBank = AF127824
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 19
 t ttc ctg gag att ggc ttc aac cta gtc att gtg ccc aaa atg ctg ggg 49
 Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu Gly
 1 5 10 15
 acc ctg ctt gcc cag gac aca acc atc tcc ttc ctt ggc tgt gcc act 97
 Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala Thr
 20 25 30
 cag atg tat ttc ttc ttc ttc ttt gga gtt gct gaa tgc ttc ctg ctg 145
 Gln Met Tyr Phe Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu Leu
 35 40 45
 gct acc gtg gca tat gac cgc tat gtg gcc atc tgc agt ccc ttg cac 193
 Ala Thr Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
 50 55 60
 tac cca gtc atc atg aac caa agg aca cgg gcc aaa ctg gct gct gcc 241
 Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala Ala
 65 70 75 80
 tcc tgg ttc cca ggc ttt cct gta gct act gtg cag acc aca tgg ctc 289

Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp Leu
85 90 95

ttc agt ttt cca ttc tgt cgc acc aac aag gtg aac cac ttc ttc tgt 337
Phe Ser Phe Pro Phe Cys Arg Thr Asn Lys Val Asn His Phe Phe Cys
100 105 110

gac agc cca cct gtg ctg agg ctg gtc tgt gca gac aca gca ctg ttt 385
Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala Asp Thr Ala Leu Phe
115 120 125

gag atc tac gcc atc gtc gga acc att ctg gtg gtc atg atc ccc tgc 433
Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro Cys
130 135 140

ttg ctg atc ttg tgt tcc tat act cgc att gct gct gcc atc ctc aag 481
Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu Lys
145 150 155 160

atc cca tca gct aaa ggg aag aat aaa gcc ttt tct aca cgt tcc tca 529
Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser
165 170 175

cac ctc ctt gtt gtc tct ctt ttc tat ata tca tta agc ctc aca tat 577
His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr Tyr
180 185 190

ttt cgg cct aaa tca aat aat tct cct gag ggc aag aag ctg cta tcg 625
Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu Ser
195 200 205

ttg tcc tac act gtt atg act ccc 649
Leu Ser Tyr Thr Val Met Thr Pro
210 215

<210> 20

<211> 216

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9598; gene = PTR12; Accession DDBJ/EMBL/GenBank = AF127824

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20 25 30

Gln Met Tyr Phe Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu Leu

35 40 45
 Ala Thr Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
 50 55 60
 Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala Ala
 65 70 75 80
 Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp Leu
 85 90 95
 Phe Ser Phe Pro Phe Cys Arg Thr Asn Lys Val Asn His Phe Phe Cys
 100 105 110
 Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala Asp Thr Ala Leu Phe
 115 120 125
 Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro Cys
 130 135 140
 Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser
 165 170 175
 His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr Tyr
 180 185 190
 Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu Ser
 195 200 205
 Leu Ser Tyr Thr Val Met Thr Pro
 210 215

<210> 21
 <211> 650
 <212> DNA
 <213> Pan troglodytes
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 <222> (1)..(650)

<223> Taxon = 9598; gene = PTR2; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127825

<400> 21

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ccacccttta cattacacag caaagatgac ccatcagctc tgtgccctgc tggttgctgg      240
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attctgtgca gacaatgcca tcctcactt cttctgcgat gtgactccc tactgaaact      360
ctcctgtcga gacacacacc tcaatgaggt cataatcctt agtgaggggtg ccctgggtcat      420
gatcacccca tttcttttga tcctggcttc ttatatgcac atcacctgca ctgtcctgag      480
ggtcccatcc acaaagggaa ggtggtaagc cttctccacc tgtggctctc acctggctgt      540
ggttctacct cttctatggc accatcattg ctgtgtattt taaccctctg tcctccact      600
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<210> 22

<211> 649

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9598; gene = PTR3; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127826

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tgcagtggca gaaacattca tgctggcagt gatggcctat gattgatacg tggcagtggt      180
taaccctttg ctctacacag ttgtcagggtc ccagaaactc tgtgcatcat tagtggcagg      240
gccctacaca tgggggtataa tctcttctct gacactcacc tatttcctct tgtcattatc      300
cttctgtggg tctaacatca tcaataatth tgtctgtgag gactctgtca tcctctctgt      360
ctcctgtctc gaccctaca tcagccaaat gctttgtttt gtcattgcaa tattcaatga      420
ggtgagcagc ttgggagtca tcctcactac ctatatthtc atctttattg ctgtcataaa      480
aatgccttct gctgttgggc accaaaaagc tttctctacc tgtgcttccc acctgactgc      540
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atggctcata gtcaaagtag gttctgtgtt ttatacagtc atcatcccc 649

<210> 23
<211> 651
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(651)
<223> Taxon = 9598; gene = PTR4; pseudogene; Accession DDBJ/EMBL/ GenBank =
AF127827
<400> 23

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gttgtttgct tattttatgg gaaaggcatt ggggggtacc tgagttcaga tgtgtcatct 600
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<210> 24
<211> 657
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(657)
<223> Taxon = 9598; gene = PTR5; pseudogene; Accession DDBJ/EMBL/ GenBank =
AF127828
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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctattaccgc tttgtggcca 180

tctgtcaccc tatatatcat tcaaccatca tgaacccgtg tttctgtggc tttctagttt 240
tggtgtcttt ttttttttct cagtctttta gacgcccagc tgcacaactt gattgcctta 300
caaatgacct gcttcaagga tgtggaaatt cctaatttct tctgggaacc ttctcaactt 360
ccccatcttg catgttgca caccctcacc aataacataa tcatgtattt ccctgctgcc 420
atatttggtt ttcttcccat ctgggggacc cttttctctt attataagat tgtttcctcc 480
attctgaggg tttcatcatc aggtgggaag tataaggcct gctccacctg tgggtctcac 540
ctgtcagttg tttgctgatt ttatggaaga tgcgttggag ggtacctcag ttcagatgtg 600
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<210> 25

<211> 657

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(657)

<223> Taxon = 9598; gene = PTR6; pseudogene; Accession DDBJ/EMBL/GenBank = AF127829

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acaaacgacc tgcttcaagg atgtggaaat tctaatttct ttctgtgatc cttctcaact 360
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<210> 26

<211> 650

<212> DNA

<213> Pan troglodytes

<220>
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<222> (1)..(650)
<223> Taxon = 9598; gene = PTR7; pseudogene; Accession DDBJ/EMBL/GenBank = AF127830
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tggcctgttc tgacacctcc attaataaca tggttgtata ttttattggt gccatatttg 420
gttttctccc tctcttaggg atccttttct ctactataa aattgtttcc tccattctga 480
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cctccaggaa ggggtgcagtg gcctcagtga tgtacatggt ggtcaccccc 650

<210> 27
<211> 663
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(663)
<223> Taxon = 9598; gene = PTR8; pseudogene; Accession DDBJ/EMBL/GenBank = AF127831
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tctgtcaccc tctatatcgt tcagccatct tgaaccctg tttctgtggc tttctaggtt 240
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tgccttacia atgacctgct tcaaggatgt ggaaattcct aatttcttcc gggaaccttc 360
tcaactcccc catcttgcat gttgtgacac cttcactagg aacatcaaca tgtattttct 420
tgctgccata tttggttttc ttcccatctc ggggaccctt ttctcttact gtaaaattgt 480

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gatgtgtcat cttccccgag aaaggggtgca gtggcctcag tgatgtacac ggtggtcacc 660
ccc 663

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<210> 28
<211> 677
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(677)
<223> Taxon = 9598; gene = PTR9; pseudogene; Accession DDBJ/EMBL/Genbank =
AF127832
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ggtacctcag ttcagatgtg tcacttccc ccagaaaggg tgcagtggcc tcagtgatgt 660
acacggtggt caccccc 677

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<210> 29
<211> 643
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 9580; gene = HLA45; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127833

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gcatgtatag aagacatgct cctgactctg atggcctatg accgatttgt ggccatctgt      180
caccctctgc actaccagtc catcgtgaat cctcacctct gtgtcttctt agttttgttg      240
tcttttttcc ttagcctggt ggattcccag ctacacagct ggattgtggt tacaattcac      300
cttcttcaag aatggaaatc tctaattttt tctgtgacct gtctcaactt ctcaaccttg      360
cctgttctga cagcatcatc gataacatat tatatattta gatagcccta tatttggttt      420
tcttccatt tcagggatcc ttttgtctta gtataaaatt gtctcccca ttccgagaat      480
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tgcattttat gaaacaggca ttggcgtgta cctgacttca gctgtgtcat catccccag      600
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<210> 30
<211> 648
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 9580; gene = HLA46; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127834
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648

<210> 31

<211> 660

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(660)

<223> Taxon = 9580; gene = HLA47; pseudogene; Accession DDBJ/EMBL/GenBank = AF127835

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ctcccccatc ttgcatgttg tgacaccttc accaataaca taatcatgta ttttctgtct 420

gccgtatttg gggtccttcc catctcgggg accctttcct cttactataa aatgggtttcc 480

tccattctga ggctttcatc gtcagggtgg aagtataaag cttctccac ctgtgggtct 540

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<210> 32

<211> 649

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9580; gene = HLA48; Accession DDBJ/EMBL/GenBank = AF127836

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 32

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5

10

15

aac atc cag acc aag aac aaa gcc atc tcc tac atg gac tgc ctc aca 97

Asn	Ile	Gln	Thr	Lys	Asn	Lys	Ala	Ile	Ser	Tyr	Met	Asp	Cys	Leu	Thr		
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Gln	Val	Tyr	Phe	Ser	Met	Leu	Phe	Pro	Ile	Leu	Asp	Thr	Leu	Leu	Leu		
		35					40				45						
acc	gtg	atg	gcc	tat	gac	cgg	ttt	gtg	gcc	atc	tgc	cac	cct	ctg	cac	193	
Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu	His		
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tac	atg	atc	atc	atg	aac	ccc	cgc	ctc	tgt	ggc	ctc	ctg	att	ttt	gtc	241	
Tyr	Met	Ile	Ile	Met	Asn	Pro	Arg	Leu	Cys	Gly	Leu	Leu	Ile	Phe	Val		
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Ile	Trp	Leu	Ile	Gly	Val	Met	Thr	Ser	Leu	Leu	His	Ile	Ser	Leu	Met		
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Met	His	Leu	Ile	Phe	Cys	Lys	Asp	Phe	Glu	Ile	Pro	His	Phe	Phe	Cys		
			100					105					110				
gaa	ctg	aca	cac	atc	ctc	cag	ctg	gcc	cgc	tct	gat	acc	ttc	ctg	aac	385	
Glu	Leu	Thr	His	Ile	Leu	Gln	Leu	Ala	Arg	Ser	Asp	Thr	Phe	Leu	Asn		
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agc	acg	ttg	ata	tac	ttt	atg	aca	ggg	gtg	ctg	ggc	gtt	ttt	ccc	ctc	433	
Ser	Thr	Leu	Ile	Tyr	Phe	Met	Thr	Gly	Val	Leu	Gly	Val	Phe	Pro	Leu		
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Met	Ser	Ser	Ser	Gly	Gly	Lys	Gln	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser		
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cac	ctc	tcc	gtt	gtt	tct	tta	ttt	tat	ggg	aca	ggc	att	ggg	gtc	cac	577	
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Gly	Ile	Gly	Val	His		
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Phe	Thr	Ser	Ala	Val	Thr	His	Ala	Ser	Gln	Lys	Ile	Ser	Val	Ala	Ser		
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<210> 33
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<212> PRT
<213> Hylobates lar
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<223> Taxon = 9580; gene = HLA48; Accession DDBJ/EMBL/GenBank = AF127836
<400> 33
Trp Val Asp Ile Cys Phe Gly Thr Cys Ile Ile Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
65 70 75 80

Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Arg Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 34
 <211> 649
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9580; gene = HLA5; Accession DDBJ/EMBL/GenBank = AF127837
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 34
 c tgg gtt gac atc tgt ttc agc act tgc atc atc ccc aag atg ctg gtg 49
 Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Ile Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag acc aag aac aaa gcc atc tcc tac atg gac tgc ctc aca 97
 Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30
 cag gtc tat ttc tcc atg ctt ttt cct att ctg gac acg cta ctc ctg 145
 Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45
 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc ctc cct ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His
 50 55 60
 tac atg atc atc atg aac ccc cgc ctc tgt ggc ctc ctg att ttt gtc 241
 Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
 65 70 75 80
 atc tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg 289
 Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
 85 90 95
 atg cat cta atc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337
 Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
 100 105 110
 gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385
 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

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agc acg ttg ata tac ttt atg aca ggt gtg ctg ggc gtt ttt ccc ctc      433
Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
    130                135                140

ctt ggg atc att ttc tct tat tca cga att gct tca tcc ata agg aag      481
Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
    145                150                155                160

atg tcc tca tct ggg gga aaa caa aaa gca ctt tcc acc tgt ggg tct      529
Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
                165                170                175

cac ctc tcc gtt gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
                180                185                190

ttc act tct gca gtg act cac gct tcc cag aaa atc tcc gtg gcc tcg      625
Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
                195                200                205

gtg atg tac acg gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
    210                215

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<210> 35

<211> 216

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9580; gene = HLA5; Accession DDBJ/EMBL/GenBank = AF127837

<400> 35

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Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Ile Pro Lys Met Leu Val
1                5                10                15

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Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
                20                25                30

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Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
    35                40                45

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His
    50                55                60

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Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
    65                70                75                80

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Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 36

<211> 651

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(651)

<223> Taxon = 9580; gene = HLA6; pseudogene; Accession DDBJ/EMBL/GenBank = AF127838

<400> 36

cttgccctgac atcggtttca ccaccaccac ggtccccgag atgattgtgg acatccaatc 60

tcacagcaga gtcattctcct aggcaggccg cctgactcac atgtctctct ttgccatttt 120

tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgacagg tttgtagcca 180

tctgtcacc tctatatcat tcagccatca tgaacccgtg tttctgtggc tttctagttg 240

tctttttttt ctctcagtct ttttagaggcc cagctgcata acttgattgc cttgctaattg 300
acctgcttca aggatgtgga aattcctaataa ttcctctgtg acccttctca actccgccat 360
cttgcatgtt gtgacatctt caccaataac ataatcatgt attttcctgc tgccgtattt 420
gggttccttc ccattctcggg gaccctttcc tcttactata aaatgggttc ctccattctg 480
aggctttcat cgtcagggtg gaagtataaa gccttctcca cctgtgggtc tcacctgtca 540
gttgtttgct gagtttatgg aagaggcggt ggagggtacc tcagttcaga tgtgtcctct 600
tccccagaa agtttgcagt ggcctcagt atgtacacgg tggtcacccc c 651

<210> 37

<211> 644

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(644)

<223> Taxon = 9580; gene = HLA7; pseudogene; Accession DDBJ/EMBL/GenBank = AF127839

<400> 37

ctgggctgac atcactttca cctcgcccat ggttcccaag atgattgtgg acatgcagtc 60
gcatagcaga gccatctctt atgcaggctg cctgacacag atgtctttct ttgtcctttt 120
tgcatgtatg gaagacatgc tcctgactct gatggcctat gaccgatttg tggccatctg 180
tcacccctg cactaccag tcatcgtgaa tcctcacctc tgtgtcttct tagttttgtt 240
gtcttttttc cttagcctgt tggattccca gctacacagc tggattgtgt ttacaatcca, 300
ccttcttcaa gaatggaaat ctctaatttt ttctgtgacc cgtctcaact tctcaacctt 360
gcctgttctg acagcatcat cgataacata ttatatattt agatagccct atatttggtt 420
ttcttcccat ttcagggatc cttttgtctt agtataaaat tgtctcccc attctgagaa 480
ttccatcgtc agatgggaag tataaagcct tctccacctg tggctctcac ctggcagttg 540
ttgcatttta tgaaacaggc attggcgtgt acctgacttc agctgtgtca tcatcccca 600
ggaatgggtgt ggtggcgta gtgatgtatg ctgtgggtcac cccc 644

<210> 38

<211> 649

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

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<222> (1)..(649)
<223> Taxon = 9580; gene = HLA74; Accession DDBJ/EMBL/GenBank = AF127840
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 38
c ttt gtt gat ttc tgt tat tct act acg att aca ccc aaa ctg ctg gag      49
  Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
    1             5             10             15

aac ttg gtt gtg gaa tat aga act att tcc ttc aca gga tgc atc atg      97
  Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
            20             25             30

caa ttc ttc ctt gtc tgc ata ttt gta ggg aca gaa aca ttc atg ctg      145
  Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu
            35             40             45

gca gtg atg gcc tat gac cga tgt gtg gcg gtg tgt aac cct ctt ctc      193
  Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu
    50             55             60

tac aca gtt gca atg tcc cag agg ctt tgc tcc ttg ttg gtg gct aca      241
  Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
    65             70             75             80

tca tac tct tgg ggg ata gtc tgt ttc ctg aca ctt acc tac ttt cta      289
  Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu
            85             90             95

ctg gaa tta tcc ttc aga gga aat aat atc att aat aac ttt gtc tgt      337
  Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
            100            105            110

gag cat gct gcc att gtt gct gtg tct tgc tct gac ccc tat gtg agc      385
  Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser
            115            120            125

cag gag atc act tta gtt tct gcc aca ttc aat gaa ata agc agt ctg      433
  Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
            130            135            140

atg atg att ttc act tcc tat gct ttc att ttt atc act gtc atg aag      481
  Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
    145            150            155            160

atg cct tcc act ggg ggg cgc aag aaa gcg ttc tcc acg tgt gcc tcc      529
  Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
            165            170            175

cac ctg acc gcc att acc att ttc cat ggg act atc ctt ttc ctc tac      577
  His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
            180            185            190

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tgt	gtt	cct	aac	tcc	aaa	agt	tca	tgg	ctc	atg	gtc	aag	gtg	acc	tct	625
Cys	Val	Pro	Asn	Ser	Lys	Ser	Ser	Trp	Leu	Met	Val	Lys	Val	Thr	Ser	
		195					200					205				

gtc ttt tac aca gtg ttc att ccc
Val Phe Tyr Thr Val Phe Ile Pro
210 215

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<210> 39
<211> 216
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA74; Accession DDBJ/EMBL/GenBank = AF127840
<400> 39
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Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
1 5 10 15

Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
20 25 30

Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu
50 55 60

Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
65 70 75 80

Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu
85 90 95

Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
100 105 110

Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser
115 120 125

Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
130 135 140

Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
145 150 155 160

Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
180 185 190

Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Thr Ser
195 200 205

Val Phe Tyr Thr Val Phe Ile Pro
210 215

<210> 40

<211> 659

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(659)

<223> Taxon = 9580; gene = HLA75; pseudogene; Accession DDBJ/EMBL/GenBank = AF127841

<400> 40

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tcacagcaga gtcattctct aggcaggccg cctgactcag atgtctctct ttgccatttt 120
tggaggcatg gaagagagac atgctcctga gtgtgacggc ctatgaccgg tttgtagcta 180
tctgtcacc tctatatcat tcagccatca tggaccctg tttctgtgac ttcttagttt 240
tggtgtcttt tttttttctt ctcatgtttt tcgactccca gctgcacaac ttgattgcct 300
tgctaattgac ttgcttcaag gatgtggaaa ttcctaattt cttctgtgac ccttctcaac 360
tccccatct tgcattgtgt gacagcatca ccaataacgt catcatgtat ttccctgctg 420
ccgtatttgg tttccttccc atctcgggga cccttttctc ttgctataaa atcgtttcct 480
ccattctgag ggtttcatca tcaggtggga ggtataaagc cttctccacc tgtgggtctc 540
acctgtcagt tgtttgtgga gtttatggaa gaggtgttgg agggtaacct agttcagggt 600
tgtcatcttc cccagaaaag ggtgcagtgg cctcagtgat gtacacggtg gtcaccccc 659

<210> 41
<211> 662
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(662)
<223> Taxon = 9580; gene = HLA8; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127842
<400> 41

gtcacctgac gtcggtttca cctccaccac ggtccccgag atgattgtgg acacccattc 60
tcacagcaca gtcattctct aggcaggctg cctgactcag atgcctctct ttgccatttt 120
tggaggcatg gaagagagac aagctcctga gtgtgatggc ctatgaccgg tttgtagcca 180
tctgtcacc ctttatatcgt tcagccatca tgaatccgtg tttctgtggc tacctagttt 240
tggtgtcttt tttttttttt ttgcgagtcg tttagactcc cagctgcaca acttgattgc 300
cttgctaata acctgcttca gggatgcgga aattcctaata ttcttctgtg acccttctca 360
actcccccat cttgcatggt gtgacacctt caccaataac ataatacatg tatttccctg 420
ctgccatatt tggtttcctt cccatctcgg ggaccctttt ctctttctgt aaaattgttt 480
cctccgttct gaggggttca tcgtcaggta ggaagtataa agccttctcc acctgtgggt 540
ctcacctgtc agttgtttgc tgagtttatg gaagaggcgt tggagggtac gtcagttcag 600
atgtgtcttc tttccccaga aagggtgcag tggcctcagt gatgtacatg atggtcaccc 660
cc 662

<210> 42
<211> 662
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(662)
<223> Taxon = 9593; gene = GGO1; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127843
<400> 42

cttgactgac atcggtttca cctccaccac agtccccaaag atgattgtgg acatccagtc 60
tcacagcaga gccattctct atgcacgctg cctgactcag atgtctctct ttgccatttt 120
tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca 180
tctgtcacc cttgtatcgt ccagccatct tgaaccctg tttctgtggc ttcttagatt 240
cgttgtcctt gttttttttt tttttttctc agtcttttag actcccagct gcacaacttg 300

attgccttac aaatgacctg cttcatggat gtggaaattc ctaatttctt ctgggaacct 360
tctcaactcc cccatcttgc atgttgtgac accttcacca ggaacatcaa cctgtatttc 420
cctgctgccca tatttggttt tcttcccatc tcggggaccc ttttctctta ctataaaatt 480
gtttcctcca ttctgaaggt ttcacaggt gggaagtata aaccttctcc gcctgtggtt 540
ctcacctgtc agttgtttac tgattttatg gaacaggcgt tggagggtac ctcggttcag 600
atgtgtcatc tccccgaga aagggtgcag tggcctcagt gatgtacacg gtggtcaccc 660
cc 662

<210> 43
<211> 650
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 9593; gene = GG017; pseudogene; Accession DDBJ/EMBL/ GenBank =
AF127844
<400> 43

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acagaacaaa ttcataacat atgcaggctg tctcggtcag attttttttt ttcacttcat 120
ttggatgcct ggacaattta ctcttgactg tgatggccta tgaccgcttc gtggccatct 180
gtcaccacct gcactatacg gtcacatga acccccggt ctgtggactg ctggttctgg 240
ggctctggtg catcagtgtc atgggttccc tgctcgagac cttgactgtt ttgaggctgt 300
ccttctgcac caaaatggaa attccacact ttttttgtga tcttcttgaa gtctgaagc 360
tcgcctgttc tgacaccttc attaataacg tggatgata ctttgcaact ggcgctctgg 420
gtgtgattcc cttcactgga atatttttct cttactataa aattgttttc tctatactga 480
ggatttcctc agctgggaga aagcacaagg cggtttccac ctgtggttcc cacctctcag 540
tggtcacctt gttctatggc acgggctttg gggctctatct cagttctgca gccacacat 600
cttctaggac aagtctggtg gcctcagtga tgtacacat ggtcaccccc 650

<210> 44
<211> 649
<212> DNA
<213> Gorilla gorilla
<220>

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<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GG018; Accession DDBJ/EMBL/GenBank = AF127845
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 44
c ttc gta gac atc tgt ttt gtc tct acc act gtc ccg aag atg ctg gtg      49
  Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
    1             5             10             15

aac atc cag aca cac aac aaa gtc atc acc tat gca ggc tgc atc acc      97
Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
    20             25             30

cag atg tgc ttt ttc tta ctc ttt gta gga ttg gat aac ttc ctt ctg      145
Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu
    35             40             45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac cct ctg cac      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
    50             55             60

tac atg gtc att atg aac cct caa ctc tgt gga ctg ctg gtt ctg gcg      241
Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
    65             70             75             80

tcc tgg atc gtg ggt gtt ctg aat tcc atg tta caa agc tta atg gtg      289
Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val
    85             90             95

ttg cca ctg ccc ttt tgt aca cac atg gaa atc cct cat ttt ttc tgt      337
Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Phe Cys
    100            105            110

gaa att aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat      385
Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
    115            120            125

gac ata gtg atg tat ttt gca gta gca ctg ctg ggc ggt ggt ccc ctc      433
Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Gly Pro Leu
    130            135            140

aat ggg atc ctg tac tct tac tct aag ata gtt tcc tcc ata cgt gca      481
Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
    145            150            155            160

atc tca tca gct cag ggg aag tat aag gca ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
    165            170            175

cac ctc tca gtt gtc tcc tta ttt tat ggt aca tgc tta ggg gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu Gly Val Tyr

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180 185 190
 ctt agt tct gct gca acc cac aat tca cac aca ggt gct gca gcc tca 625
 Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala Ala Ala Ser
 195 200 205

 gtg atg tac act gtg gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

 <210> 45
 <211> 216
 <212> PRT
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9593; gene = GGO18; Accession DDBJ/EMBL/GenBank = AF127845
 <400> 45
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

 Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30

 Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu
 35 40 45

 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

 Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

 Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val
 85 90 95

 Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Phe Cys
 100 105 110

 Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

 Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Gly Pro Leu
 130 135 140

Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 46

<211> 649

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9593; gene = GGO19; Accession DDBJ/EMBL/GenBank = AF127846

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 46

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 Phe Val Asp Ile Cys Phe Ile Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act 97
 Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
 20 25 30

cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg 145
 Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
 35 40 45

gct gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac 193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca 241
 Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tct tgg ttc atc att ttc tgg ttc tcg ctg gtt cat gtt cta ctg atg 289
 Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met
 85 90 95

aag agg ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt 337
 Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat 385
 Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
 115 120 125

aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta 433
 Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
 130 135 140

gct ggg atc ctc ttc tcc tac tct cag att gtc tcc tcc tta atg aga 481
 Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
 145 150 155 160

acg tcc tcc acc aag ggc aag tac aaa gcc ttt tcc acc tgt gga tct 529
 Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cac ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat 577
 His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

ctg agt tct gct gtg acc cat tct tcc cag agc agc tcc atg gcc tca 625
 Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Met Ala Ser
 195 200 205

gtg atg tac gcc atg gtc acc ccc 649
 Val Met Tyr Ala Met Val Thr Pro
 210 215

<210> 47

<211> 216

<212> PRT

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9593; gene = GGO19; Accession DDBJ/EMBL/GenBank = AF127846

<400> 47

Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
 20 25 30

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met
 85 90 95

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
 130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
 145 150 155 160

Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
 195 200 205

Val Met Tyr Ala Met Val Thr Pro
 210 215

<210> 48
 <211> 649
 <212> DNA
 <213> Gorilla gorilla
 <220>

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<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO2; Accession DDBJ/EMBL/GenBank = AF127847
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 48
c ttt gta gac atc tgt gtt acc tcc acc aca gtc cca aag aca ctg tca      49
  Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
    1             5             10             15

aac atc cgg aca cag agc aaa gtc atc acc tat gca ggt tgc atc acc      97
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
      20             25             30

cag atg tac ttt ttt ata ctc ttt gta gtg ttg gac agc tta ctc ctg      145
Gln Met Tyr Phe Phe Ile Leu Phe Val Val Leu Asp Ser Leu Leu Leu
      35             40             45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50             55             60

tac aca gtc att atg aac tcc tgg ctc tgt gga ctg ctg gtt ctg gtg      241
Tyr Thr Val Ile Met Asn Ser Trp Leu Cys Gly Leu Leu Val Leu Val
      65             70             75             80

tcc tgg atc gtg agc atc cta tgt tct ccg tta caa agc ata atg gca      289
Ser Trp Ile Val Ser Ile Leu Cys Ser Pro Leu Gln Ser Ile Met Ala
      85             90             95

ttg cag ctg tcc ttc tgt aca gaa ttg aaa atc cct cat ttt ttc tgt      337
Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His Phe Phe Cys
      100            105            110

gaa ctt aat cag gtc gtc cac ctt gcc tgt tct gac act ttt att aaa      385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Ile Lys
      115            120            125

gac atg atg atg aat ttt aca agt gtg ctg ttg ggt ggg gga tgc ctc      433
Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu
      130            135            140

gct gga ata ttt tac tct tac ttt aag ata ctt tgt tgc ata tgt tca      481
Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser
      145            150            155            160

atc tca cca gct cag ggg atg aat aaa gca ctt tcc acc tgt gca tct      529
Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser
      165            170            175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc gta ggt gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr

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                180                185                190
ctt agt tct gct gca acc cat aac tca ctc tca aat gct gca gcc tca      625
Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser
                195                200                205

gtg atg tac acc gtg gtc acc tcc      649
Val Met Tyr Thr Val Val Thr Ser
                210                215

<210> 49
<211> 216
<212> PRT
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO2; Accession DDBJ/EMBL/GenBank = AF127847
<400> 49
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
1                5                10                15

Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
                20                25                30

Gln Met Tyr Phe Phe Ile Leu Phe Val Val Leu Asp Ser Leu Leu Leu
                35                40                45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
                50                55                60

Tyr Thr Val Ile Met Asn Ser Trp Leu Cys Gly Leu Leu Val Leu Val
65                70                75                80

Ser Trp Ile Val Ser Ile Leu Cys Ser Pro Leu Gln Ser Ile Met Ala
                85                90                95

Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His Phe Phe Cys
                100                105                110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Ile Lys
                115                120                125

Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu
130                135                140

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Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser
 145 150 155 160

Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Ser
 210 215

<210> 50
 <211> 649
 <212> DNA
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9593; gene = GGO3; Accession DDBJ/EMBL/GenBank = AF127848
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 50
 c ttt gtg gac acc tct ttc atc tcc acc aca gtc ccc aag atg cta gtg 49
 Phe Val Asp Thr Ser Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act 97
 Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
 20 25 30
 cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg 145
 Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
 35 40 45
 gcc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac 193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca 241
 Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

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tct tgg ttc atc att ttc tgg ttc tcc ctg gtt cat att cta ctg atg      289
Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
           85                      90                      95

aag aag ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt      337
Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
           100                      105                      110

gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat      385
Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
           115                      120                      125

aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta      433
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
           130                      135                      140

gct ggg atc ctc ttc tcc tac tct cag att gtc tcc tcc tta atg aga      481
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
           145                      150                      155                      160

acg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc acg ctg tgg atc      529
Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
           165                      170                      175

tcc ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat      577
Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
           180                      185                      190

ctg agt tct gct gtg acc cac tct tcc cag agc agc tcc atg gcc tca      625
Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
           195                      200                      205

gtg atg tac gcc gtg gtc acc ccc      649
Val Met Tyr Ala Val Val Thr Pro
           210                      215

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<210> 51

<211> 216

<212> PRT

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9593; gene = GGO3; Accession DDBJ/EMBL/GenBank = AF127848

<400> 51

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Phe Val Asp Thr Ser Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1           5           10           15

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Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20           25           30

```

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
 85 90 95

Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
 130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
 145 150 155 160

Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
 165 170 175

Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
 195 200 205

Val Met Tyr Ala Val Val Thr Pro
 210 215

<210> 52
 <211> 650
 <212> DNA
 <213> Gorilla gorilla
 <220>

<221> misc_feature
<222> (1)..(650)
<223> Taxon = 9593; gene = GGO4; pseudogene; Accession DDBJ/EMBL/GenBank = AF127849

<400> 52
cttggctgag attggtttca tctcggtcgc ggttcccaag atgacgtgg acatgcagtc 60
acatagcaga gtcattctct atgcgggccc cctgacacag atgtctttct ttgtcctttt 120
tgcatgtatg gatgacatgc tccggactct gatggcctat gaccgatttg tggccatctg 180
tcaccccctg cactaccag tcattcatgaa tcctcacctc tgtgtcttct tagtttttgt 240
gccttttttc cttagcctgt tggattccca gctgcacagc tggattgtgt tacaattcac 300
ttgcttcaag aatgtggaaa tatctaattt tttatgtgat ccatctcaac ttctcaaact 360
tgactgttct gaacagtgtc atcaatagca tttcacata tttagatagt actatgtttg 420
gtttccttcc catttcaggg atccttttgt cttactataa aattgtccc tccattctaa 480
gaattccatc gtcagatggg aagtataaag ccctctccac ctgtggtctt cacctgtcag 540
ttgtttgctt attttatgga ataggcattg gcgtgtacct gacttcagct gtgtcaccac 600
caccaggaa tgggtgtgtg gcatcagtga tctacgcggt ggtcaccccc 650

<210> 53
<211> 650
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 9593; gene = GGO70; pseudogene; Accession DDBJ/EMBL/GenBank = GenBank = AF127850

<400> 53
cttgccctgac atcggtttca cctccaccat ggtccccaag atgattgtgg acgtccaatc 60
tcacagcagg ttcattctct atgcaggctg cctgactcag atatctctct ttgccatttt 120
tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca 180
tctgtcacc cttatatcat tcagccatca tgaaccctg tttctgtggc ttcttagatt 240
tgctgtcttt tttttctttc tttttctcag tcttttagat ggtagctgc agaacttgat 300
tgccttacia atgacctgct tcgaggatgt gggaattcct aatttcctct gtgaccttc 360
tcaactgccc catctcacat gttgtgacat cttaccaat cacataatca tgtatttccc 420
tgctgccata tttggttttc tcccatctc ggggacctt ctctcttacc atgtaattgt 480

ttcctccatt ctgagggttt catcatctat gggagggtga aagccttccc cacctgtgag 540
 ttgtttgctg atattatgga acaggcttcg gagggtacct cagttcagat gtgttatctt 600
 caacaagaaa ggctgcagtg gcctcagtga tgtacacggt ggtcacgccc 650

<210> 54
 <211> 649
 <212> DNA
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9593; gene = GGO71; Accession DDBJ/EMBL/GenBank = AF127851
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 54
 t ttt gct gac ctc tgt ttt acc tcc acg act gtc cca aag atg tta ctg 49
 Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Leu
 1 5 10 15
 aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt 97
 Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
 20 25 30
 cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg 145
 Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45
 act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg 241
 Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
 65 70 75 80
 tcc tgg tgc atc agt gtc atg ggt tcc ctg ctc gag acc ttg act gtt 289
 Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
 85 90 95
 ttg agg ctg tcc ttc tgc acc aaa atg gaa att cca cac ttt ttt tgt 337
 Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 gat ctt ctt gaa gtc ctg aag ctc gcc tgt tct gac acc ttc att aat 385
 Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 aac gtg gtg ata tac ttt gca act ggc gtc ctg ggt gtg att ccc ttc 433
 Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe

130 135 140
 act gga ata ttt ttc tct tac tat aaa att gtt ttc tct ata ctg agg 481
 Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
 145 150 155 160
 att tcc tca gct ggg aga aag cac aaa gcg ttt tcc acc tgt ggt tcc 529
 Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc tca gtg gtc acc ttg ttc tat ggc acg ggc ttt ggg gtc tat 577
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
 180 185 190
 ctc agt tct gca gcc aca cca tct tct agg aca agt ctg gcg gcc tca 625
 Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Ala Ala Ser
 195 200 205
 gtg atg tac acc atg gtc acc ccc 649
 Val Met Tyr Thr Met Val Thr Pro
 210 215

 <210> 55
 <211> 216
 <212> PRT
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9593; gene = GGO71; Accession DDBJ/EMBL/GenBank = AF127851
 <400> 55
 Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Leu
 1 5 10 15

 Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
 20 25 30

 Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

 Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
 65 70 75 80

 Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys
 100 105 110

Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe
 130 135 140

Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Ala Ala Ser
 195 200 205

Val Met Tyr Thr Met Val Thr Pro
 210 215

<210> 56

<211> 649

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 13515; gene = EFU35; Accession DDBJ/EMBL/GenBank = AF127852

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 56

c ctc act gac atc tgt tta agc aca gcc acc gtc cca aag atg ctg gca 49
 Leu Thr Asp Ile Cys Leu Ser Thr Ala Thr Val Pro Lys Met Leu Ala
 1 5 10 15

aac atc cga aca cgg agt cag agc atc acg tat gca gcc tgc ctc acc 97
 Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr
 20 25 30

cag atg tgc ttt gtt ctg ggt tct gct acg ttg gaa aat ttt ctc ctg 145
 Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu
 35 40 45
 gca gta atg gct tat gac cgc tat gtg gcc atc tgt cat cct ctg aga 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
 50 55 60
 tac gcg gtc atc atg aac ctt cgt ctc tgt ggc ttc ttg atc ctt ttg 241
 Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu
 65 70 75 80
 tcc ctg tct att agc atc atg gac acc ctg ctc cac gat ctg atg gtc 289
 Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val
 85 90 95
 ttg cgg ctg tcc ttc tgc aca cac ctg gag ata ccc ctc ttc ttc tgc 337
 Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys
 100 105 110
 gag gtt gtg caa gtc atc aag ctt gcc tgt tct gat acc ctc atc aat 385
 Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn
 115 120 125
 aac ctc ttg ata tat ttt gca gct ggc gtg ttg gga ggt gtt cct ctg 433
 Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu
 130 135 140
 tct ggg atc att ttc tct tat act cag att gcc tcc tct gtt ttg aga 481
 Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg
 145 150 155 160
 atg gca tca gca agt gga aag tat aaa gct ttt tcc acc tgt ggc tct 529
 Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc tcg gtt gtg tcc ttg ctc tac ggg aca ggt ttg ggg gtg tac 577
 His Leu Ser Val Val Ser Leu Leu Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190
 atc agt tct gcg ttt atg cac tct ccc agg acg atg gca gtg gct tca 625
 Ile Ser Ser Ala Phe Met His Ser Pro Arg Thr Met Ala Val Ala Ser
 195 200 205
 atg atg tac acg gtg gtc act ccc 649
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 57

<211> 216

<212> PRT

<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 13515; gene = EFU35; Accession DDBJ/EMBL/GenBank = AF127852
<400> 57
Leu Thr Asp Ile Cys Leu Ser Thr Ala Thr Val Pro Lys Met Leu Ala
1 5 10 15

Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr
20 25 30

Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
50 55 60

Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu
65 70 75 80

Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys
100 105 110

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn
115 120 125

Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu
130 135 140

Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg
145 150 155 160

Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Leu Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Ile Ser Ser Ala Phe Met His Ser Pro Arg Thr Met Ala Val Ala Ser

195

200

205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 58
 <211> 645
 <212> DNA
 <213> Eulemur fulvus
 <220>
 <221> misc_feature
 <222> (1)..(645)
 <223> Taxon = 13515; gene = EFU36; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127853
 <400> 58
 ctttgctgac gtctgtttca cctccaccac ggtgcccaag atgttagtga acatccaggc 60
 gcacagcaag gccatcacat acaaaggctg cctcaccag atgtgttttt tcttgatttt 120
 tgggtgggcta gtttgctact gacggtgatg gcctatgacc gggtcgtggc catctgtcac 180
 cccctgcgct acatgggtcat catgaacccc aggctctgtg gtcttctgct tctcctttct 240
 tggttgatct gcttgacgta ttctctgtg caaagtctga tggttttgag ggtgtccttc 300
 tgccaagaaa tagaaatccc ccactacttc tgtgaacttg ctcagatcct cagctcgcc 360
 tgctctgaca ccctagttaa tgacgtcctg ctgtattttc tatctgctct gctcgggtgtt 420
 attcccctga ctgggatacct ttattcttat tccagaatta tctcctccat aatgtgcatt 480
 tcctctgctg gaggggaagta caaagccttt tccacctgtg ggtctcacct ctccgctcgc 540
 tccttgttct acggtacagg ccttggggctg tacctaactt ctgaaacagc ccagccctcc 600
 agaaggggtt caatagcctc ggtgatgtac accatgggtca ccccc 645

<210> 59
 <211> 647
 <212> DNA
 <213> Eulemur fulvus
 <220>
 <221> misc_feature
 <222> (1)..(647)
 <223> Taxon = 13515; gene = EFU37; pseudogene; Accession DDBJ/EMBL/GenBank = AF127854
 <400> 59
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 tcacagcaga gtcactcctt ctgggggctg tctgaccag atgtctcttg ctctgctttt 120

tgtttgtgtg gatgatatgc ttctgaccgt gtcggcctgt gacctgtttg tggccatctg 180
ccacccctg cactacacgg tcatcatgaa ccccaacttc tgtggcctcc tggttctgat 240
atcttggttc atcatgtccc tggttgtcct ggttcacctc ctactgataa ggaggctgac 300
attccccagg gccacagaaa tcccacatta cttctgtgaa ctgggtcaaa ttctcaaagt 360
ggcccaactct gacagcttca tcaataacat ctccttgtac ttgtcggctg tgttgctggg 420
tgtgtttccc atcacaggga tccctacttc ctactctaaa attgtctcct ccgtaatgag 480
gatgtcgtcc actgcaggca agaagaaagc atttccacc tgtgggtctc atttgtgtgg 540
tctgcttgtt ctatggaaca gggcttgggg tctacctcag ctctgctgtg accccttctt 600
cccagagcag cagcattgcc tcagtgatgt actcggtggt caccccc 647

<210> 60

<211> 652

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(652)

<223> Taxon = 34829; gene = ERU38; pseudogene; Accession DDBJ/EMBL/GenBank = AF127855

<400> 60

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acacagcaaa gacatctcct acgtgggatg cctcactcag atgtattttt tcatggtgtt 120
tgggtggactg gacaacttcc tctgaccgt gatggcctgt gaccggtttg tggccatctg 180
tcacccctg cactatgcag tacagtcac atgaaccccc gcttctgtgc cctcctgggt 240
ctgatgtctt gggtcatcat gtccctggat gccctgggtc atgttctact tatactgagg 300
ctgacctttt ccttagaaac tgaaatccca catttcttct gtgacctggc tcagatgctc 360
gagggtggccc gctctgacac ctttatcaat aacatctgct tgtacttggt ggctgtgttg 420
ctgtatgttt cctgtcacgg ggatcctcta cccctactct aaaattgtct cctccttaat 480
gaggatgtcc tccactgcag gcaagaagaa agcattttcc acctgtgggt ctcacctctc 540
tgtggtcctc ttgttctatg gaacaggact tggggtctac ctaagttctg ctgtgacccc 600
ttcttcccag agcagcgcca ttgcctcagt gatgtacaca gtagtcaccc cc 652

<210> 61

<211> 648

<212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(648)
 <223> Taxon = 34829; gene = ERU39; pseudogene; Accession DDBJ/EMBL/GenBank = AF127856
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gagcaaagtc atatcctaca caggctgcat caccagatg gactttttct tgctctttgt      120

aggactggac aacttcctcc tgaccgtgat ggcctgtgac cggtttgtgg ccatctgtca      180

ccccctgcac tatgcagtac agtcatcatg aaccccaggc tctgtgcatt tcttgttctg      240

gtgttctgga tcctgagtgt cctgaattcc ttgttacaaa gcttaatggg gttgcagata      300

accttctgta cagacttgga aatccccac tttttctgtg aacttaatca gataatccac      360

cttgccgtgt tggacacctt tcttaatgac atggatgatg atttggcagt gatgctgctg      420

gggtgggggt gccttactgg gatcctttac tcttactcta agatagtttc ctccgtacgt      480

gcaatctcct cggctcaggg gaagtataaa gcattttcca cctgtgcata tcacctctcg      540

gtcgtctcct tattttattg tacatgccta ggggtgtacc tcagttctgc tacacacaac      600

tcacactcca gcgcaacagc ctcggtgatg tacacgggtg tcaactccc      648

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<210> 62
 <211> 649
 <212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 34829; gene = ERU40; Accession DDBJ/EMBL/GenBank = AF127857
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 62

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  Leu Ser Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
    1             5             10             15

aac ctt cac gca cac agc aaa gac atc tcc tac agg gag tgc ctc act      97
  Asn Leu His Ala His Ser Lys Asp Ile Ser Tyr Arg Glu Cys Leu Thr
    20             25             30

cag gtg tat ttt ttt atg att ttt gct gga ctg gat aat ttc ctc ctg      145
  Gln Val Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu

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35	40	45	
acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac			193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His			
50	55	60	
tac atg gtc atc atg aat ccc cgc ttc tgt gcc ctc ctg gtt ctc atg			241
Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met			
65	70	75	80
tct tgg ttc atc atg tct ctg gtt gcc ctg gtt cat gtt cta ctt ata			289
Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile			
	85	90	95
ttg agg ctg act ttt tcc tta gaa act gaa atc cca cat ttc tcc tgt			337
Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys			
	100	105	110
gag gtg gct cag att ctc aag gtg gcc cgc tct gac acc ttc ttc aat			385
Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn			
	115	120	125
aac atc tgc tta tac ttg tgc gct gtg ttg ctg ggt gtg ttt ccc gtc			433
Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val			
	130	135	140
atg ggg atc ctc ttc tcc tac tct aaa att gtt tca tcc tta atg agg			481
Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg			
145	150	155	160
atg tcc tcc act tca gca aag aat aaa gca ttt tcc acc tgt ggg tct			529
Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser			
	165	170	175
cac ctc tgt gtg gtc tct ttg ttc tat gga act gca ctt ggg gtc tac			577
His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr			
	180	185	190
ctc agc tct gct gtg acc cct tct tcc cag agc agc gcc att gcc tca			625
Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ala Ile Ala Ser			
	195	200	205
gtg atg tac acg gtg gtc acc ccc			649
Val Met Tyr Thr Val Val Thr Pro			
210	215		

<210> 63
 <211> 216
 <212> PRT
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(649)

<223> Taxon = 34829; gene = ERU40; Accession DDBJ/EMBL/GenBank = AF127857

<400> 63

Leu Ser Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
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Asn Leu His Ala His Ser Lys Asp Ile Ser Tyr Arg Glu Cys Leu Thr
20 25 30

Gln Val Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met
65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile
85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys
100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn
115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val
130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg
145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ala Ile Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 64
<211> 648
<212> DNA
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 13515; gene = EFU56; pseudogene; Accession DDBJ/EMBL/GenBank = AF127858
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tgcagagtag gcactttcct cctgactgtg atggcctatg actggtttgg ggccatctgt 180
caccacctgc actatgtgct catcatgaac cccaggctct gtgcactgct tgttctggtg 240
tcctggatca tgagtgtcct gaattccttg ttgcaaagct taatggtgtt gccactgccc 300
ttctgtgcag agttggaaat ccccagttt ttctgtgaac ttaatcagat aatcctcctt 360
gcctgttctg acacctttct taatgacgtg gtgatgtatt tggcagctat gctactgggt 420
gaggggtgcc ttactgggat cctttactct tactctaaga tagtttcctc cgtacgtgca 480
atctcctcgg ctcaggggaa gtataaagca tttccacct gtgcacttca cctctcggtc 540
gtctccttat ttactgcac aagcctcggg gtgtacctcg gctctgctgc tacacacaac 600
tcacactoca gcgcaacagc ctcggtgatg tacacgggtg tcactccc 648

<210> 65
<211> 643
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 13515; gene = EFU57; Accession DDBJ/EMBL/ GenBank = AF127859
<220>
<221> CDS
<222> (2)..(643)
<223> Product = olfactory receptor
<400> 65
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Phe Ala Asp Ile Cys Phe Val Ser Thr Val Pro Glu Met Leu Asn
1 5 10 15

gtg cag aca tgg agc aaa gtc ata tct tac aca ggc tgc atc acc cag	97
Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln	
20 25 30	
atg gac ttt ttc ttg ctc ttt gta gga ctg gac aac ttc ctc ctg acc	145
Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr	
35 40 45	
gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cgc tat	193
Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr	
50 55 60	
gca gtc atc atg aac ccc agg ctc tgt gta ttt ctt gtt ctg gtg tcc	241
Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser	
65 70 75 80	
tgg atc ctg agt gtc ctg aat tcc ttg tca caa agc tta atg gtg ttg	289
Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu	
85 90 95	
cgg cta acc ttc tgt aca gac ttg gaa atc ccc cac ttt ttc tgt gaa	337
Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu	
100 105 110	
ctt aat cag ata atc cac ctt gcc tgt tgc gac acc ttt ctt aat gac	385
Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp	
115 120 125	
gtg gtg atg tat ttg gca gtg atg ctg ctg ggt ggg gga tgc ctt act	433
Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Gly Cys Leu Thr	
130 135 140	
ggg atc ctt tac tct tac tct aag ata gtt tcc tcc gta cgt gca atc	481
Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile	
145 150 155 160	
tcc tcg gct cag ggg aag tgt aaa gca ttt tcc acc tgt gca tct cac	529
Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His	
165 170 175	
ctc ttg gtc gtc tcc tta ttt tat tgt aca tgc cta ggg gtg tac ttg	577
Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu	
180 185 190	
agt tct gct aca cac aac tca cac tcc agc gca aca gcc tcg gtg atg	625
Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met	
195 200 205	
tac acg gtg gtc act ccc	643
Tyr Thr Val Val Thr Pro	
210	

<211> 214
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 13515; gene = EFU57; pseudogene; Accession DDBJ/EMBL/GenBank = AF127859
<400> 66
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1 5 10 15

Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln
20 25 30

Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr
35 40 45

Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
50 55 60

Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser
65 70 75 80

Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu
85 90 95

Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu
100 105 110

Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp
115 120 125

Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Gly Cys Leu Thr
130 135 140

Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile
145 150 155 160

Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His
165 170 175

Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu

180

185

190

Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met
195 200 205

Tyr Thr Val Val Thr Pro
210

<210> 67
<211> 644
<212> DNA
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(644)
<223> Taxon = 34829; gene = ERU66; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127860
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acagagcaaa tccatcaccg gtgccggctg cctcacacag atgtactgtt tcatggcttt 120
tggacttctg gacaatctga tgctgatggt catggcttat gaccactttg tggccatctg 180
tcaccctctg cactacacag tcatcatgaa cccagtgtc tgtgtccagg tgcttgtcca 240
caccgggctt gtcagcatcc tgggggcctt cctcggagag tgaccgtgtt ggggcttctt 300
ttggtgcagt cactgaaatc ccacactatt tctgtgagct ccctgaggct ctccagctct 360
cccactctga cccctccatc aataatgtca tattatacat tgtgacgggt tcatgggctt 420
ctttctctct gctgagattc ttttctctta ttctccaact gttttttctg tcttgaggat 480
ctcaacagca ggggggaagt ataaagtgtt ttcctcctgt gagtctcacc tctcggttgt 540
ctgcctgttc tgtgggacct gcctggggtc tagctcagtt ccacatggac acacgcttct 600
ccgacagggg tgttgccctg gtcccataca ctgtagtcac cccc 644

<210> 68
<211> 649
<212> DNA
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 34829; gene = ERU67; Accession DDBJ/EMBL/GenBank = AF127861
<220>
<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 68

t ttc atg gat atc tgc ttc aca aca gtc att gtg ccc aag atg ctg gtg	49
Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val	
1 5 10 15	
aat ttc ctg tca gag aca aag gcc atc tcc tat gtg ggc tgt ctg gtc	97
Asn Phe Leu Ser Glu Thr Lys Ala Ile Ser Tyr Val Gly Cys Leu Val	
20 25 30	
cag atg tac ttc ttc atg gcc ctt gca aac act gac agc tac cta ctg	145
Gln Met Tyr Phe Phe Met Ala Leu Ala Asn Thr Asp Ser Tyr Leu Leu	
35 40 45	
gcc tcc atg gct att gac cgg ctg gtg gcc atc tgc aaa ccc ttc cac	193
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Lys Pro Phe His	
50 55 60	
tat gat gtg gtt atg agc cca cgg cgt tgc ctc ctc atg ctg ttg ggt	241
Tyr Asp Val Val Met Ser Pro Arg Arg Cys Leu Leu Met Leu Leu Gly	
65 70 75 80	
tct tgc acc atc tcc cac cta cac tcc ctg ttc cgg gtg cta ctc atg	289
Ser Cys Thr Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met	
85 90 95	
tct cgc ctg tct ttc tgt gcc tcc cac atc att aag cac ttt ttc tgt	337
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys	
100 105 110	
gat acc cag cct gtg cta aag ctt tcc tgc tct gac aca tcc tcc agc	385
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser	
115 120 125	
cag att gtg gtc atg acc gag acc ctg gct gtc atc gtg acc ccc ttc	433
Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe	
130 135 140	
ctg tgc atc atc ttc tcc tat ctg aga atc atc atc act gtg ctc gca	481
Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Ala	
145 150 155 160	
atc ccc tct gca gcc ggg aag tgg aag gcc ttc tcc acc tgt ggc tcc	529
Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser	
165 170 175	
cac ctc act gtg gtg gtc ctg ttc tat ggc agt gtc atc tat gtg tat	577
His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr	
180 185 190	
ttc agg ccc ctg tcc atg tac tca gtg atg aag gac cgg gta gcc aca	625
Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Asp Arg Val Ala Thr	
195 200 205	

gtt atg tac acg gta gtg aca cct
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 69
<211> 216
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 34829; gene = ERU67; Accession DDBJ/EMBL/GenBank = AF127861
<400> 69
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1 5 10 15

Asn Phe Leu Ser Glu Thr Lys Ala Ile Ser Tyr Val Gly Cys Leu Val
20 25 30

Gln Met Tyr Phe Phe Met Ala Leu Ala Asn Thr Asp Ser Tyr Leu Leu
35 40 45

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Lys Pro Phe His
50 55 60

Tyr Asp Val Val Met Ser Pro Arg Arg Cys Leu Leu Met Leu Leu Gly
65 70 75 80

Ser Cys Thr Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
85 90 95

Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
115 120 125

Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
130 135 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Ala
145 150 155 160

Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr
 180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Asp Arg Val Ala Thr
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 70

<211> 649

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 13515; gene = EFU83; Accession DDBJ/EMBL/GenBank = AF127862

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 70

c ttt tct gac atc tgc ttg gtc tgc acc act gtc cca cag atg ctg gtg 49
 Phe Ser Asp Ile Cys Leu Val Ser Thr Val Pro Gln Met Leu Val
 1 5 10 15

aat gtg cag aca cac agc aaa gtc ata tcc tac gca ggc tgc gtc acc 97
 Asn Val Gln Thr His Ser Lys Val Ile Ser Tyr Ala Gly Cys Val Thr
 20 25 30

cag atg gac ttc ttt gta ctc ttt gta ggg ctg gac agc ttc ctc ctt 145
 Gln Met Asp Phe Phe Val Leu Phe Val Gly Leu Asp Ser Phe Leu Leu
 35 40 45

acc gtg atg gcc tat gac cgg ttt gtg gtc atc tgc cac cca ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Val Ile Cys His Pro Leu His
 50 55 60

tac gcg gtc acc atg aac ccc agg ctg tgt ggg ctg ctg gtg ctg ctg 241
 Tyr Ala Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Leu
 65 70 75 80

tct tgg atc atg agt gcc ctg agt tcc ttg tta gaa agc tta gtg gtg 289
 Ser Trp Ile Met Ser Ala Leu Ser Ser Leu Leu Glu Ser Leu Val Val
 85 90 95

ctg tgg gtg tgc ttc tgt ctg gac ttg gaa atc ccc cac ttt ttc tgt 337
 Leu Trp Val Cys Phe Cys Leu Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

 gaa ctt aat gag ata atc cac ctg gcc tgt tct gac acc ttt ctt att 385
 Glu Leu Asn Glu Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Ile
 115 120 125

 gac atg gtg atg tat ttc tca gct cta ctg ctg ggt ggt ggt tcc ctg 433
 Asp Met Val Met Tyr Phe Ser Ala Leu Leu Leu Gly Gly Gly Ser Leu
 130 135 140

 gct ggg atc ctt tac tct tac tct aag ata gtt tcc tcc gta cgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala
 145 150 155 160

 atc tcc tca gct cag ggg aag tat aaa gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

 cac ctc gcg gtt gtc tcc cta ttt tac tgc aca agc ctc ggg gtg tac 577
 His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
 180 185 190

 ttg agt tct gct gct aca cac aac tca cac tcc agc gca aca gcc tcg 625
 Leu Ser Ser Ala Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser
 195 200 205

 gtg atg tac acg gtg gtc act ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 71

<211> 216

<212> PRT

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 13515; gene = EFU83; Accession DDBJ/EMBL/GenBank = AF127862

<400> 71

Phe Ser Asp Ile Cys Leu Val Ser Thr Thr Val Pro Gln Met Leu Val
 1 5 10 15

Asn Val Gln Thr His Ser Lys Val Ile Ser Tyr Ala Gly Cys Val Thr
 20 25 30

Gln Met Asp Phe Phe Val Leu Phe Val Gly Leu Asp Ser Phe Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Val Ile Cys His Pro Leu His
 50 55 60

Tyr Ala Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Leu
 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Ser Ser Leu Leu Glu Ser Leu Val Val
 85 90 95

Leu Trp Val Cys Phe Cys Leu Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Glu Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Ile
 115 120 125

Asp Met Val Met Tyr Phe Ser Ala Leu Leu Leu Gly Gly Gly Ser Leu
 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala
 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 72

<211> 642

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(642)

<223> Taxon = 34829; gene = EFU84; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127863

<400> 72

ctttgtagac atctgttttg tctctacat ggtcccaaag atgctggtga acatcaagac 60
acacagcagt catatcctat gcaggctgtg tcaccagat gcacttttcc ataatctttg 120
cagagttaga catcttcctc ctgacggtga tggcctatga ccggtgtgtg gccatctgtc 180
acccctgca ctacacggcc atcatgaacc ccaggctctg tgaactgctg gttctggctt 240
cctggatcat aagtggcccg aattccttgt tacaaagtgt aaaggctgtg tggctgtcct 300
tctgtacaaa cttggaaatc cgtcactttt tctgtgaact tagatactac atcttgctg 360
ttgtgacacc tctgttcctg acgtggtgat acatattgca gctgtggtgc tggctgtttt 420
tcctcttgct gggatccttt actcttactc tcagatagtt tcctccacac gtgcaacttc 480
ctcagctcag gcgaagtgtg aagcattttc cacctgtgca gctcacctcg cggttgtctc 540
tctattttac tgcacaagcc tcggggtgtg cttgagctct gctgctacac acaaccaca 600
ctccagcgca acagcctcgg tgatgtacat ggtggtcact cc 642

<210> 73

<211> 652

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(652)

<223> Taxon = 13515; gene = EFU86; pseudogene; Accession DDBJ/EMBL/GenBank =

AF127864

<400> 73

ctttgcagac atctgttttg gttccaccac tgtcccaaag atgctggtga atgtgcagac 60
acagagcaaa gtcatactct acgcaggctg cgtcacccag atggactttt tcatactctt 120
tgcagggttg gatatcttta tgctgatcat gatggcctat gaccggtttg gggccatctg 180
tcaccactg cagtacacgg tcatcatgaa cccaggtc tgtgggctgc tggttgtggt 240
gccctggatc ttgagtgacc tgaattcctt gttacaaagc ttaatggtgt tgtcactgtc 300
cttttgtaga cacttggaat tcctcacttt ttctgtgaac ttaatcaggt tgtccacctt 360
gcctgttctg aaaccttctt taatgacatg gtgatgtatc tgatatctgt ggtgctgggt 420
ggtggttccc tggctgggac tctttattct ttcttactgc agaatagttt gctccatagc 480
tgcaacgtcc tcagctcagg ggaagtataa agcatttccc acctgtgcat ctcacctctc 540
agttgtctcc ttatcttctc gcacaatcct aggggtgtac ctcagctctg ctgctaccca 600
gaattcgtgc tccagtgcag tagccttggt ggtgtacag gtggtcactc cc 652

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<210> 74
<211> 649
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 13515; gene = EFU87; Accession DDBJ/EMBL/GenBank = AF127865
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 74
c ttt gtt gac atc tgt ttc acc tcc acc acc atc ccc aag atg ctg gtg      49
  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
    1             5             10             15

aac att gaa aca cac agc aaa gac atc tcc tac atg gga tgc ctc act      97
Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
      20             25             30

cag atg tat ttt ttc atg att ttt gct gga ctg gat aat ttc ctc ctg      145
Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
      35             40             45

act gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc tta cac      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50             55             60

tac acg gtc atc atg agt ccc cgc ttc tgt gcc ctc ctg gtt ctc ata      241
Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
      65             70             75             80

tct tgg ttc atc atg acc ctg gtt gcc ctg gtt cat gta cta ctg ata      289
Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile
      85             90             95

ttg agg ctg acc ttc tct tta gaa act gaa atc cca cat ttc ttc tgt      337
Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Phe Cys
      100            105            110

gac ctg gct cag att ctc gag gtg gcc cac tct gat acc ctc atc aat      385
Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn
      115            120            125

aac atc tgc atg tac ttg tgc act gtg ttg ctg ggc gtg ttt cct gtc      433
Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val
      130            135            140

acg ggg atc ctc ttc tcc tac tct aaa att gtc tcc tcc tta atg agg      481
Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg
      145            150            155            160

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atg tcc tcc act gca ggc aag aag aaa gca ttt tcc acc tgt ggg tct 529
Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

cac ctc tct gtg gtc tgc ttg ttc tgc gga aca gga gtt ggg gtc tat 577
His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr
180 185 190

ctc agt tct gct gtg acc cct tct tcc cag agc agc agc att gcc tca 625
Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser
195 200 205

gtg atg ttc acg gtg gtc acc ccc 649
Val Met Phe Thr Val Val Thr Pro
210 215

<210> 75

<211> 216

<212> PRT

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 13515; gene = EFU87; Accession DDBJ/EMBL/GenBank = AF127865

<400> 75

Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
1 5 10 15

Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
65 70 75 80

Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile
85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn
 115 120 125

Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val
 130 135 140

Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg
 145 150 155 160

Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser
 195 200 205

Val Met Phe Thr Val Val Thr Pro
 210 215

<210> 76

<211> 646

<212> DNA

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 9546; gene = MSY1; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127866

<400> 76

ctttgttgac atctgtttta tctcaccac cgtcccagg atgctgatga acatccaggc 60

atggagcaaa gacatctcct acgtggggtg cctcactcag gtgtattttt taatgatgtt 120

tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg 180

ccacccctg cactacacgg tcatcatgaa ccctgcctc tgtggcctcc tggttctggc 240

atcttgattc atcattttat ggggtctcct agttcatatt ctactgatga agagtttgat 300

ctccataggc actgagattc cgcatttctt ctgtgaactg gctcagggtcc tcaagggtggc 360

ccgctctgat actctcctcg ttaacattgt cttgtatgtg gccacagcac tgctgggtgt 420

gcttctgtga gctgggatcc tcttctccta ctctcagatc gtctcctcct taatgaggat 480

gtcctccacc gagggcaagt gcaaagcctt ttccacctgt ggggtctcacc tctgtgtggt 540
 ctccttggtc tatggaacag gacttggggg ctatctcagt tctgctgtga cccattcttc 600
 ccagagcagc tccatggcct cagtgatgta caccatgggc accccc 646

<210> 77

<211> 649

<212> DNA

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY12; Accession DDBJ/EMBL/GenBank = AF127867

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 77

c ttc gta gac gtc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg 49
 Phe Val Asp Val Cys Phe Val Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

aac atc cag aca cag aac aaa gtc atc acc tat gca ggc tgc atc agc 97
 Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Ser
 20 25 30

cag atg tgc ttt ttc ata ttc ttt gca gga ttg gac atc ttt atg ctg 145
 Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
 35 40 45

acc gtg atg gcc tac gac agg ttt gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac acg gtc acc atg aac ccc agg ctc tgt gga ctg ctg gtt ctg gcg 241
 Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc atg agt gcc ctg aat tct tca ttg caa agc tta atg gta 289
 Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val
 85 90 95

ttg cac ctt tcc ttc tgt gca gac ttg gaa att ccc cac ttt ttc tgt 337
 Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctt aat cag gtc atc cac ctt acc tgt tct gac act ttt ctt aat 385
 Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn
 115 120 125

gac atg gtg atg tat ttg tca gct gtg ctg ctg ggt ggg gga tgt ctc 433

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu
 130 135 140

 att ggg atc ctt tac tct tac tct aag atc gtc tcc tct ata cat gca 481
 Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala
 145 150 155 160

 atc tca tca gtt cag ggg aag tac aag gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

 cac ctc tcg gtt gtc tcc tta ttt tat tgt aca atc cta ggt gtg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr
 180 185 190

 ctt agt tct gct gca acc cac agc tca cac gca agt gct gca gtc tcg 625
 Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
 195 200 205

 gtg atg tac act gtg gtt acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 78
 <211> 216
 <212> PRT
 <213> Macaca sylvanus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY12; Accession DDBJ/EMBL/GenBank = AF127867
 <400> 78

Phe Val Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Ser
 20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val

85

90

95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn
 115 120 125

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu
 130 135 140

Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala
 145 150 155 160

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 79

<211> 649

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 79

c ttg gct gac atc ggt ttc acc tcc acc aca gtc ccc aag atg ctg gtg 49
 Leu Ala Asp Ile Gly Phe Thr Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc 97
 Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser

20	25	30	
cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc			145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu			
35	40	45	
acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac			193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr			
50	55	60	
tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg			241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val			
65	70	75	80
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg			289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met			
85	90	95	
ctg cag ttg tcc ttt tgc acc agt tgg gtc att cag cac ttt tac tgc			337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys			
100	105	110	
gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat			385
Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn			
115	120	125	
tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc			433
Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe			
130	135	140	
tca gga atc ctt ttc tcc tac acc caa att gtc tcc tcc atc ctg aga			481
Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg			
145	150	155	160
atc tca tcc aca gat ggg aaa cac aaa gcc ttt tct aac tgc gga tct			529
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser			
165	170	175	
cat ctg tct gtg gtt ttt tta ttc tat ggg aca ggc ctt ggt gtg tat			577
His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr			
180	185	190	
ctt agt tcc aat gca tgc tcc tct tcc tgg cgg ggc atg gtg gcc tgc			625
Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser			
195	200	205	
gtc atg tac act gtg gtc acc ccc			649
Val Met Tyr Thr Val Val Thr Pro			
210	215		

<210> 80
 <211> 216
 <212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868

<400> 80

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
20 25 30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
100 105 110

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
115 120 125

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
130 135 140

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser
165 170 175

His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 81
<211> 647
<212> DNA
<213> *Macaca sylvanus*
<220>
<221> misc_feature
<222> (1)..(647)
<223> Taxon = 9546; gene = MSY2; pseudogene; Accession DDBJ/EMBL/GenBank = AF127869
<400> 81
cttcgtagac gtctgttttg tgtccaccac tgtcccgaag atgctgggtga acatccagac 60

acagaacaaa gtcacacact atgcaggctg catcagccag atgtgctttt tcatattctt 120

tgcaggattg gacaccttta tgctgaccgt gatggcctac gacaggtttg tggccatctg 180

tcacctctg cactacacgg tcacatgaa cccaggctc tgtggactgc tggttctggc 240

gtcctgatca tgagtgccct gaattcttca ttgcaaagct taatggtatt gcacctttcc 300

ttctgtgcag acttggaat tcccacttt ttctgtgaac ttaatcaggt catccacctt 360

acctgttctg acacttttct taatgacatg gtgatgtatt tgtcagctgt gctgctgggt 420

gggggatgtc tcattgggat cctttactct tactctaaga tcgtctcctc tatacttgca 480

atctcatcag ttcaggggaa gtacaaggca tttccacct gtgcatctca cctctcggtt 540

gtctccttat ttattgtaca atcctagggtg tgtaccttag ttctgctgca acccacagct 600

cacacgcaag tgctgcagtc tcggtgatgt aactgtggt taccccc 647

<210> 82
<211> 649
<212> DNA
<213> *Macaca sylvanus*
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 82

210

215

<210> 83
<211> 216
<212> PRT
<213> *Macaca sylvanus*
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870
<400> 83

Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Met Val
1 5 10 15

Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Val Gly Leu Asp Ile Phe Met Leu
35 40 45

Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu
130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 84
 <211> 646
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(646)
 <223> Taxon = 9546; gene = MSY6; Accession DDBJ/EMBL/GenBank = AF127871
 <220>
 <221> CDS
 <222> (2)..(646)
 <223> Product = olfactory receptor
 <400> 84
 c ttc act gac ctc ttc ttt gtc acc aac aca atc ccc aag atg ctg gtg 49
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15

 aac ctc cag tcc cag aac aaa gcc atc tcc tat gca ggg tgt ctg aca 97
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30

 cag ctc tac ttc ctg gtc tcc ttg gtg gcc ctg gac aac ctc atc ctg 145
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35 40 45

 gct gtg atg gcg tat gac cgc tat gtg gcc atc tgc tgc ccc ctc cac 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60

 tac acc aca gcc atg agc cct aag ctc tgt atc tta ctc ctt tcc ttg 241
 Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ser Leu
 65 70 75 80

 tgt tgg gtc tta tct gtg ctc tat ggc ctc ata cac acc ttc ctc atg 289
 Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
 85 90 95

 acc acg gtg acc ttc tgt ggg tca cga aaa atc cac tac atc ttc tgt 337
 Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
 100 105 110

gag atg tat gta ttg ctg agg ctg gca tgt tcc gac act cag att aat 385
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
 115 120 125

 cac aca gtg ctg att gcc aca ggc tgc ttt atc ttc ctc att ccc ttt 433
 His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
 130 135 140

 gga ttc atg atc att tcc tat gtg ttg att gtc aga gcc atc ctc aga 481
 Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
 145 150 155 160

 ata ccc tca gtc tct aag aaa tac aaa gcc ttc tcc act tgt gcc tcc 529
 Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

 cat ttg ggt gta gtc tcc ctc ttc tat ggg aca ctt cgt atg gta tac 577
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr
 180 185 190

 ctg aag ccc ctc cat acc tac tct gtg aag gac tca gta gcc aca gtg 625
 Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val Ala Thr Val
 195 200 205

 atg tat gcg gtg gtg aca ccc 646
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 85

<211> 215

<212> PRT

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 9546; gene = MSY6; Accession DDBJ/EMBL/GenBank = AF127871

<400> 85

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15

Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30

Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60

Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ser Leu
65 70 75 80

Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
85 90 95

Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
100 105 110

Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
115 120 125

His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
130 135 140

Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
145 150 155 160

Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr
180 185 190

Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val Ala Thr Val
195 200 205

Met Tyr Ala Val Val Thr Pro
210 215

<210> 86

<211> 649

<212> DNA

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 86

c tgg gtt gac atc tgt ttc agc atc tgc atc atc ccc aag atg ctg gtg 49
 Trp Val Asp Ile Cys Phe Ser Ile Cys Ile Ile Pro Lys Met Leu Val
 1 5 10 15

aac atc cag acc aag aac aaa acc atc tct tac atg gac tgc ctc acc 97
 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30

cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg cta ctc ctg 145
 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45

acc gtg atg gct tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60

tat gta acc atc atg aac ccc cgc ctc tgc ggc ctc ctg gtt ttt gtc 241
 Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
 65 70 75 80

acg tgg ctc att ggt gtc atg aca ccc ctc ctc cat att tct ctg ttg 289
 Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu
 85 90 95

acg cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337
 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385
 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

agc acg ttg ata tat gtt atg aca ggt gtg ctg ggc gtt ttt ccc ctc 433
 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
 130 135 140

ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag 481
 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160

atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529
 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175

cac ctc tcc atc gtt tct tta ttt tat ggg aca ggc att ggg gtc cat 577
 His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
 180 185 190

ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg 625
 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
 195 200 205

gtg atg tac acg gtg gtt acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro

210

215

<210> 87

<211> 216

<212> PRT

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872

<400> 87

Trp Val Asp Ile Cys Phe Ser Ile Cys Ile Ile Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
50 55 60

Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu
85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
 180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 88
 <211> 645
 <212> DNA
 <213> *Macaca sylvanus* <220> <221> misc_feature <222> (1)..(645) <223>
 Taxon = 9546; gene = MSY8; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127873
 <400> 88
 ctttgttgac atctgtttta tctccaccac cgtccccagg atgctgatga acatccaggc 60
 atggagcaaa gacatctcct acgtgggggtg cctcactcag gtgtattttt taatgatgtt 120
 tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg 180
 ccaccccctg cactacacgg tcatcatgaa cccctgcctc tgtggcatcc tggttctggc 240
 atcttgattc atcattttat gggctctcct agttcatatt ctactgatga agagtttgat 300
 ctccataggc actgagattc cgcattttct ctgtgaactg gctcagggtcc tcaagggtgcc 360
 cgctctgata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg 420
 cttcctgtag ctgggacctt cttctcctac tctcagatcg tctcctcctt aatgaggatg 480
 tcctccaccg agggcaagta caaagccttt tccacctgtg ggtctcacct ctgtgtggtc 540
 tccttgttct atggaacagg acttggggtc tatctcagtt ctgctgtgac ccattcttcc 600
 cagagcagct ccatggcctc agtgatgtac accatgggtca ccccc 645

<210> 89
 <211> 649
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY9; Accession DDBJ/EMBL/GenBank = AF127874
 <220>
 <221> CDS
 <222> (2)..(649)

<223> Product = olfactory receptor

<400> 89

c ttg gct gac atc ggt ttc acc tcc acc aca gtc ccc aag atg ctg gtg 49
 Leu Ala Asp Ile Gly Phe Thr Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc 97
 Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
 20 25 30

cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc 145
 Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
 35 40 45

acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
 50 55 60

tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg 241
 Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
 65 70 75 80

tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg 289
 Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
 85 90 95

ctg cag ttg tcc ttt tgc acc agt tgg gtc att cag cac ttt tac tgc 337
 Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
 100 105 110

gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat 385
 Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
 115 120 125

tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc 433
 Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
 130 135 140

tca gga atc ctt ttc tcc tac acc caa att gtc tcc tcc atc ctg aga 481
 Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

atc tca tcc aca gat ggg aaa cac aaa gcc ttt tct acc tgc gga tct 529
 Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cat ctg tct gtg gtt ttt tta ttc tat ggg aca ggc ctt ggt gtg tat 577
 His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

ctt agt tcc aat gca tgc tcc tct tcc tgg cgg ggc atg gtg gcc tgc 625
 Leu Ser Ser Asn Ala Ser Ser Ser Trp Arg Gly Met Val Ala Ser
 195 200 205

gtc atg tac act gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 90
<211> 216
<212> PRT
<213> *Macaca sylvanus*
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY9; Accession DDBJ/EMBL/GenBank = AF127874
<400> 90

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
20 25 30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
100 105 110

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
115 120 125

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
130 135 140

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 91

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA21; Accession DDBJ/EMBL/GenBank = AF127875

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 91

c ttt gtg gac atc tgt gtt acc tcc acc aca ctt ccg aag aca ctg tca 49
 Phe Val Asp Ile Cys Val Thr Ser Thr Thr Leu Pro Lys Thr Leu Ser
 1 5 10 15

aac atc cag aca cac agc aaa gtc atc acc tat gca ggc tgc gtc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
 20 25 30

cag ttg tac ttc ttt gta ctc ttc ata ggg ttg gac agc tta ctc ccg 145
 Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro
 35 40 45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac acg gtc atc atg aac cct cag ttc tgt gga ctg ctg gtt ctg gtg 241
 Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val
 65 70 75 80

tcc tgg atc atg agt gcc ctg cat tct ttg aca gaa agc tta atg gta 289
 Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val
 85 90 95

tac cca ctg ctc ttt tgt aca gac ttg aaa atc ccc cag ttt ttc tgt 337

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys
 100 105 110

gaa att cat cag ata att caa ttt gcc tgt tct gac acc ttt ctt aat 385
 Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

aac ctg gtg atg tat ttg tca act gtg ctc ctg ggc ggt ggt ccc ctt 433
 Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Gly Pro Leu
 130 135 140

gct ggg atc ctg tac tct tac tct aag ata gct tcc tct ata cgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
 145 150 155 160

atc tca tca gct gag ggg aag tac aag gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc cta ggg gtg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
 180 185 190

ctg agt tct gct gca acc cac agc tca ctc tca agc gca gca gcc tcg 625
 Leu Ser Ser Ala Ala Thr His Ser Ser Leu Ser Ser Ala Ala Ala Ser
 195 200 205

gtg atg tac aca gtg gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 92
 <211> 216
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA21; Accession DDBJ/EMBL/GenBank = AF127875
 <400> 92

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Leu Pro Lys Thr Leu Ser
 1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
 20 25 30

Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

50

55

60

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val
85 90 95

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys
100 105 110

Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Gly Pro Leu
130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr His Ser Ser Leu Ser Ser Ala Ala Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 93

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 93

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c ttg gtt gac atc tgt ttc acc tcc acc aca gtc ccc aag att ctg gtg      49
  Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Ile Leu Val
    1             5             10             15

aac atc cag gag cag agt ggt acc atc agc tat gca ggc tgc att gcc      97
Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
      20             25             30

cag atg tat ttt ttc atg gtt ttt gga ggc atg gac aca ttt ctc ctc      145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
      35             40             45

act gtg atg gcc tat gac cgg tat gtg gct atc tgt cac ccc ctg tcc      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
      50             55             60

tac cct gtc att gta aac ccc cgc ctc tgc ggc ctg ttg gtt ctt gtg      241
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
      65             70             75             80

tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg      289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
      85             90             95

ctg cgg cta tcc ttc tgc acc agt tgg gtc att cag cac ttt tac tgt      337
Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
      100            105            110

gag ctt gct cag gtt ctc acg ctt gcc tgc tca gac aca cat gtc aat      385
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
      115            120            125

tac atc ctg ctc tac atg gtg acc ggc ctt ctg ggc tgt gtt ccc ttc      433
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
      130            135            140

tca ggg atc ctt ttc tcc tac atc caa att gtc tcc tcc atc ctg aga      481
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
      145            150            155            160

atc cca tcc aca gat ggg aaa cat aaa gcc ttt tct acc tgt gga tct      529
Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
      165            170            175

cat ctg tct gtg gtt tct tta ttc tac ggg aca ggc ctt ggt gtc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
      180            185            190

ctt agc tcc aat gcc tcg tcc tct tcc tgg tgg ggc atg gtg gcc tca      625
Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Trp Gly Met Val Ala Ser
      195            200            205

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gcc atg tac aca gtg gtc acc cct
Ala Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 94
<211> 216
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876
<400> 94

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Ile Leu Val
1 5 10 15

Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
20 25 30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
50 55 60

Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
100 105 110

Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
115 120 125

Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
130 135 140

Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Trp Gly Met Val Ala Ser
 195 200 205

Ala Met Tyr Thr Val Val Thr Pro
 210 215

<210> 95
 <211> 649
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA23; Accession DDBJ/EMBL/GenBank = AF127877
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 95
 t ttc acg gat atc tgc ttc aca aca gtc ata gtg ccc agg atg ctg gtg 49
 Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
 1 5 10 15
 aat ttt cta tca ggg aca aag gtt atc ccc tac atg ggc tgc ctg gtc 97
 Asn Phe Leu Ser Gly Thr Lys Val Ile Pro Tyr Met Gly Cys Leu Val
 20 25 30
 caa atg tac ttc ttc atg gcc ttt ggg aac act gac agc tac ctg ctg 145
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35 40 45
 gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac 193
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60
 tat gat gtg gct atg aac ccc cgg cat tgc cta ctc atg cta ttg ggt 241
 Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Leu Gly
 65 70 75 80
 tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg 289
 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95
 tct cac ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt 337

Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
 100 105 110
 gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc 385
 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125
 cag atg gtg gtc atg act gag act tta gct gtc att gtg acc ccc ttc 433
 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140
 ctg tgt atc atc ttc tcc tac ctg cga atc atc atc act gtg ctc aga 481
 Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
 145 150 155 160
 atc ccc ttt gca gct ggg aag tgg agg gcc ttc tct acc tgt ggc tcc 529
 Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc act gta gta gcc ctt ttc tac ggg agt ata tat tat gtc tat 577
 His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr
 180 185 190
 ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca 625
 Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
 195 200 205
 gtt atg tac aca gta gtg aca ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215
 <210> 96
 <211> 216
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA23; Accession DDBJ/EMBL/GenBank = AF127877
 <400> 96
 Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
 1 5 10 15
 Asn Phe Leu Ser Gly Thr Lys Val Ile Pro Tyr Met Gly Cys Leu Val
 20 25 30
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35 40 45
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His

PCT/IB00/02017

60

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<210> 97
<211> 649
<212> DNA
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA24; Accession DDBJ/EMBL/GenBank = AF127878
<220>
<221> CDS
<222> (2)..(649)
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<223> Product = olfactory receptor

<400> 97

c ttt gta gac atc tgt ttt gtg tct acc act gtc cca aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

cag ata ggc cat tgc cta ctc ttt gca gta ttg gac gtc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
 35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg 289
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
 85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat 385
 Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt 433
 Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
 130 135 140

gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg 625
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
 195 200 205

gtg atg tac act gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 98
<211> 216
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA24; Accession DDBJ/EMBL/GenBank = AF127878
<400> 98

Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
20 25 30

Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 99

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA25; Accession DDBJ/EMBL/GenBank = AF127879

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 99

c ttt gct gac atc tgt ttc aca tcc acg acc gtc cca aag atg ctg gtg 49
 Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

gat atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc 97
 Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30

cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg 145
 Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg 241
 Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
 65 70 75 80

tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att 289
 Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
 85 90 95

ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt 337

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat 385
 Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
 115 120 125
 aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc 433
 Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
 130 135 140
 tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160
 gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct 529
 Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat 577
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190
 ctc agt ctt gca gct aca cca tct tct agg aca agt ctg atg gcc tcg 625
 Leu Ser Leu Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
 195 200 205
 gtg atg tac acc atg gtc acc ccc 649
 Val Met Tyr Thr Met Val Thr Pro
 210 215

<210> 100

<211> 216

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA25; Accession DDBJ/EMBL/GenBank = AF127879

<400> 100

Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30

Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His


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<210> 101
<211> 649
<212> DNA
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA26; Accession DDBJ/EMBL/GenBank = AF127880
<220>
<221> CDS
<222> (2)..(649)
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<223> Product = olfactory receptor

<400> 101

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c ttg gct gac att ggt ttg acc tcc acc acc gtc ccc agg aca att gtg      49
  Leu Ala Asp Ile Gly Leu Thr Ser Thr Thr Val Pro Arg Thr Ile Val
    1             5             10             15

aac att caa act cac agc aga gtc atc gcc tat gca agc tgc ctg aca      97
Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
          20             25             30

cag atg tct ttt tca atc ttt ttt gtg tgt atg gaa gac atg ctc ctt      145
Gln Met Ser Phe Ser Ile Phe Phe Val Cys Met Glu Asp Met Leu Leu
      35             40             45

gct gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac cct ctg cac      193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50             55             60

tat cca gtc atc atg agc cca cga ctc tgt ggc ttc tta gtg ttg gtg      241
Tyr Pro Val Ile Met Ser Pro Arg Leu Cys Gly Phe Leu Val Leu Val
      65             70             75             80

tct gct ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc      289
Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
          85             90             95

tta caa ttt tct tgc ttc aaa gat ata aag att tct aat ttc ttc tgt      337
Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys
          100             105             110

gac cct tct caa ctc ctc aca ctt gct tgt tcc gac acg ttt gtc aat      385
Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
          115             120             125

aac aac ata gtc atg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc      433
Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
          130             135             140

atc tca ggg atc ttt ttg tct tac tat aaa att gtt tcc tcc att ctg      481
Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
      145             150             155             160

aga gtt cca tca tca agt ggg aag tat aaa gcc ttc tct acc tgt agc      529
Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
          165             170             175

tct cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc ctt gga gtg      577
Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
          180             185             190

tac ctt ggg tca tca gtg tca tcc ccc agg aag aga gtg gtg acc tca      625
Tyr Leu Gly Ser Ser Val Ser Ser Pro Arg Lys Arg Val Val Thr Ser
          195             200             205

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gtg atg tac aca gtg gtc act ccc
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 102
<211> 216
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA26; Accession DDBJ/EMBL/GenBank = AF127880
<400> 102

Leu Ala Asp Ile Gly Leu Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1 5 10 15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20 25 30

Gln Met Ser Phe Ser Ile Phe Phe Val Cys Met Glu Asp Met Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Pro Val Ile Met Ser Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
115 120 125

Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
130 135 140

Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
145 150 155 160

Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
 165 170 175

Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
 180 185 190

Tyr Leu Gly Ser Ser Val Ser Ser Pro Arg Lys Arg Val Val Thr Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 103

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA62; Accession DDBJ/EMBL/GenBank = AF127881

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 103

c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag acg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Thr Leu Val
 1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

cag ata ggc cat tgc ctc ctc ttt gca gta ttg gac gtc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
 35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg 289
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
 85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

gta ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat 385
 Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt 433
 Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
 130 135 140

gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg 625
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
 195 200 205

gtg atg tac act gtg gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 104
 <211> 216
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA62; Accession DDBJ/EMBL/GenBank = AF127881
 <400> 104

Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Thr Leu Val
 1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His

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<210> 105
<211> 649
<212> DNA
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882
<220>
<221> CDS
<222> (2)..(649)
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<223> Product = olfactory receptor

<400> 105

t ttc acg gat atc tgc ttc aca aca gtc ata gtg ccc agg atg ctg gtg 49
 Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
 1 5 10 15

aat ttt cta tca gag aca aag gtt atc tcc tac atg ggc tgc ctg gtc 97
 Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val
 20 25 30

cca atg tac ttc ttc atg gcc ttt gcg aac act gac agc tac ctg ctg 145
 Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu
 35 40 45

gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac 193
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60

tat gat gtg gct atg aac tcc cgg cgt tgc cta ctc atg cta ttg ggt 241
 Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly
 65 70 75 80

tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg 289
 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95

tct cgc ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt 337
 Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
 100 105 110

gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc 385
 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125

cag atg gtg gtc atg act gag acc tta gct gtt att gtg acc ccc ttc 433
 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140

ctg tgt atc atc ttc tcc tac ctg cga atc atc atc act gtg ctc aga 481
 Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
 145 150 155 160

atc ccc tct gca gcc ggg aag tgg agg gcc ttc tct acc tgt ggc tcc 529
 Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cac ctc act gta gta gcc ctt ttc tac ggg agt att att tat gtc tat 577
 His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
 180 185 190

ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca 625
 Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
 195 200 205

gtt atg tac aca gta gtg aca ccc
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 106
<211> 216
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882
<400> 106

Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
1 5 10 15

Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val
20 25 30

Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu
35 40 45

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
50 55 60

Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly
65 70 75 80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
85 90 95

Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
115 120 125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
130 135 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
145 150 155 160

Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
 180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 107
 <211> 649
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA81; Accession DDBJ/EMBL/GenBank = AF127883
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 107
 c ttt gct gac atc tgc ttc aca tcc acg acc gtc cca aag atg ctg gtg 49
 Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 gat atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc 97
 Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30
 cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg 145
 Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45
 acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg 241
 Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
 65 70 75 80
 tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att 289
 Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
 85 90 95
 ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt 337

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat 385
 Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
 115 120 125
 aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc 433
 Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
 130 135 140
 tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160
 gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct 529
 Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat 577
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190
 ctc agt tct gca gct aca cca tct tct agg aca agt ctg atg gcc tcg 625
 Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
 195 200 205
 gtg atg tac acc atg gtc acc ccc 649
 Val Met Tyr Thr Met Val Thr Pro
 210 215
 <210> 108
 <211> 216
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA81; Accession DDBJ/EMBL/GenBank = AF127883
 <400> 108
 Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30
 Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

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50              55              60
Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
65              70              75              80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
85              90              95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
100             105             110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
115             120             125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
130             135             140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
145             150             155             160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
165             170             175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180             185             190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
195             200             205

Val Met Tyr Thr Met Val Thr Pro
210             215

<210> 109
<211> 649
<212> DNA
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA82; Accession DDBJ/EMBL/GenBank = AF127884
<220>
<221> CDS
<222> (2)..(649)

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<223> Product = olfactory receptor

<400> 109

c ttt gct gac atc tgt ttc aca tcc acg acc gtc cca aag atg ctg gtg 49
 Phe Ala Asp Ile Cys Phe Thr Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

ggt atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc 97
 Gly Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30

cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg 145
 Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg 241
 Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
 65 70 75 80

tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att 289
 Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
 85 90 95

ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110

gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat 385
 Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
 115 120 125

aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc 433
 Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
 130 135 140

tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160

gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct 529
 Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat 577
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

ctc agt tct gca gct aca cca tct tct agg aca agt ctg atg gcc tcg 625
 Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
 195 200 205

gtg atg tac acc atg gtc acc ccc
Val Met Tyr Thr Met Val Thr Pro
210 215

649

<210> 110
<211> 216
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA82; Accession DDBJ/EMBL/GenBank = AF127884
<400> 110
Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Gly Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
20 25 30

Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
65 70 75 80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
115 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
145 150 155 160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
195 200 205

Val Met Tyr Thr Met Val Thr Pro
210 215

<210> 111
<211> 658
<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(658)
<223> Taxon = 9600; gene = PPY10; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127885
<400> 111

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tcacagcaga gtcatttcct aggcaggcta cctgactcag atgtctctct ttgccatttt 120
tggaggcgtg gaagagagac atgctcctga gtgtgaaggc ctatgaccgg tttgtagcca 180
cctgtcaccc tctgtatcat tcagccatca tgaagtcattg tttctgtggc tttctagttt 240
tggtgtcttt tttttttctc tcagtctttt agacgcccaa ctgcacaact tgattgcctt 300
gcaaattggcc tgctttgagg atgtggaaat ttctaatttc ttctgtgacc cttctcaact 360
cccatccttg catgttgtga cagcttcacc gataacatca tcacgtatct ccctgacgcc 420
atatccccct ttattcccat ctgggggacc cttttctcta taatatcaaa ttgtttcctc 480
cattctgagg gcttcatcat cagggtggag gtataaagcc ttctccatct gtgggtctca 540
cctgtcagtt gtttgcttat tttatggaac aggcataatg gggtacctca gttcagatgt 600
gtcatcttcc ctgagaaagg ctgcagtac ctgagtgtg tacaccgtgg tcaccccc 658

<210> 112
<211> 649
<212> DNA
<213> Pongo pygmaeus
<220>

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<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY11; Accession DDBJ/EMBL/GenBank = AF127886
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 112
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  Leu Ala Asp Ile Gly Phe Thr Ser Thr Val Pro Lys Met Ile Val
    1             5             10             15

gac atg caa act cac agc aga gtc atc tcc tat gca ggc tgc ctg act      97
Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
    20             25             30

cag atg tct ttt ttt gtc ctt ttt gca tgt atg gat gac atg ctt ctg      145
Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu
    35             40             45

agt gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac cct ccg gat      193
Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp
    50             55             60

tac cca gtt acc atg aac cca tgt ttc tgt ggc ttc cta gtt ttg ttg      241
Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu
    65             70             75             80

tct ttt ttt ctc agt ctt tta gac tcc cag ctg cac aat tgg att gcc      289
Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala
    85             90             95

tta caa att acc tgc ttc aag gat gtg gaa att ccc aat ttc ttc tgt      337
Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys
    100            105            110

gac cct tcc caa ctc ccc cac ctt gcc tgt tgt gac acc ttc acc aat      385
Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn
    115            120            125

gac ata gtc atg tat ttc ctt gct gcc ata ttt ggt ttt ctt ccc atc      433
Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile
    130            135            140

ttg ggg atc ctt ttc tct tac tat aaa att gtt tcc tcc att ctg agg      481
Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg
    145            150            155            160

gtt tca tca tca ggt ggg agg tat aaa gcc ttc gcc acc tgt ggc tct      529
Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser
    165            170            175

cac ctg tca gtt gtt tgc tta ttt tat gga aca gcc ctt gga ggg tac      577
His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr

```

120

180

185

190

ctc agt tca gac atg tcc tct tat ccc aga aag ggt gca gtg gct tca 625
Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser
195 200 205

gtg atg tac aca gtg gtc acc ccc 649
Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 113

<211> 216

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9600; gene = PPY11; Accession DDBJ/EMBL/GenBank = AF127886

<400> 113

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
1 5 10 15

Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu
35 40 45

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp
50 55 60

Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu
65 70 75 80

Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala
85 90 95

Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn
115 120 125

Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile
130 135 140

Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr
 180 185 190

Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 114
 <211> 654
 <212> DNA
 <213> Pongo pygmaeus
 <220>
 <221> misc_feature
 <222> (1)..(654)
 <223> Taxon = 9600; gene = PPY12; pseudogene; Accession DDBJ/EMBL/ GenBank =
 AF127887
 <400> 114
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 cagcagagtc atctcctctg caggcttgcc tgactcagat gtctctttgc catttttgga 120
 ggcacggaag agagacatgc tcctgagtgt gatggcctat gaccggtttg tagccatctg 180
 tcaccctcta tatcattcag tcatcatgag cccgtgtttc tgtggcttcc tagttttggt 240
 gtcttttttt ttcttctcag tcttttagac tcccagctgc accacttgat tgccttgcta 300
 atgacctact tcaaggatgt ggaaattccg aatttcttct gtgaccttc tcaactcccc 360
 catattgcat gttgtgatgc cttcaccaat aacatcatca tgtatttccc tgtcaacatg 420
 tttgcttttc ttcccatctc ggggactctt ttctcttact ctaatattgt ctctccatt 480
 ctgaggggtt cgtcatcagg tgggaaatat aaagccctct ccacctgtgg gtctcactgg 540
 tcagttgttt gctgagcttc tggaacaggc gttggagggt acctcagttc agatgtgtca 600
 tcttccccca gaaaggggtgc agtggcctca gtgatgtgca ccgtgggtcac cgcc 654

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<210> 115
<211> 649
<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY49; Accession DDBJ/EMBL/GenBank = AF127888
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 115
c ttt gtg gac acc tgt ttc atc tcc acc aca gtc ccc aag atg cta gtg      49
  Phe Val Asp Thr Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
    1             5             10             15

aac atc cag gca cgg agc aaa gaa atc tcc tac atg ggg tgc ctc act      97
Asn Ile Gln Ala Arg Ser Lys Glu Ile Ser Tyr Met Gly Cys Leu Thr
      20             25             30

cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg      145
Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
      35             40             45

gct gtg atg gct tat gac cgg ttt gtg gcc atc tgc cac ccc ctt cag      193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Gln
      50             55             60

tac gcg gtc atc atg aac ccc cat ctc tgt ggc ctg ctg gtt ctg gca      241
Tyr Ala Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala
      65             70             75             80

tct tgg ttc atc att ttc tgg gtc tcc ctg gtt cat att cta ctg atg      289
Ser Trp Phe Ile Ile Phe Trp Val Ser Leu Val His Ile Leu Leu Met
      85             90             95

aag agg ctg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt      337
Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
      100            105            110

gaa ctg gct cag gtc ctc aag gtg gcc cgc tct gat acc ctc ctc aat      385
Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn
      115            120            125

aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta      433
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
      130            135            140

gct ggg atc ctc ttc tcc tac tct cag atc gtc tcc tcc tta atg aga      481
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
      145            150            155            160

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atg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc acc tgt gga tct      529
Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
              165              170              175

cac ctc tgt gtg gtc tcc ttg ttc aat gga aca gga ctt ggg gtc tat      577
His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr
              180              185              190

ctc agt tct gct gtg acc cat tct tcc cag agc agc tcc atg gcc tca      625
Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
              195              200              205

gtg atg tat gcc atg gtc acc ccc      649
Val Met Tyr Ala Met Val Thr Pro
              210              215

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<210> 116

<211> 216

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9600; gene = PPY49; Accession DDBJ/EMBL/GenBank = AF127888

<400> 116

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Phe Val Asp Thr Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1              5              10              15

```

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Asn Ile Gln Ala Arg Ser Lys Glu Ile Ser Tyr Met Gly Cys Leu Thr
              20              25              30

```

```

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
              35              40              45

```

```

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Gln
              50              55              60

```

```

Tyr Ala Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala
65              70              75              80

```

```

Ser Trp Phe Ile Ile Phe Trp Val Ser Leu Val His Ile Leu Leu Met
              85              90              95

```

```

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
              100              105              110

```

Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Thr Leu Leu Asn
 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
 130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
 145 150 155 160

Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
 195 200 205

Val Met Tyr Ala Met Val Thr Pro
 210 215

<210> 117

<211> 659

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(660)

<223> Taxon = 9600; gene = PPY50; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127889

<400> 117

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tcacagcaga gtcattctct atgcaggctg cctgactcag atgtgtctcc tggccatttt 120

tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgagcgg tttgtagccc 180

tctgtcacc cctatattct tcagccatct tgaaccctg tttctgtggc ttcctagatt 240

tgtggtcttt gttttctttt tcctcagtct tttagactcc cagctgcgca acttgattgc 300

ttacgcatga cctgcttcaa ggatgtggaa attcctaatt tcttctggga accttctcaa 360

ctcccccatc ttacattttg tgacaccttc accagtaaca tccacatgta tttcctgct 420

gccgtatttg gttttcttcc catctcgggg gcccttttct cttacggtaa aattgtttcc 480

tccattctga gggtttcatc atcaggtggg aagatcaac cttctccacc tgtgggtctc 540
acctgtcagt tgtttgctga ttttacggaa caggcggttg agggtagctg gggtcagatg 600
tgtcatcccc ccgagaaaag ggtgcagtgg cctcagtgat gtacacggtg gtcaccccc 659

<210> 118

<211> 648

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 9600; gene = PPY51; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127890

<400> 118

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tgcaggattg gacatctttc tctgactgt gatggcctat gacggtttgt ggccatctgt 180
caccacctgc actacacggt catcatgagc cccaggctct gtggactgct ggttctggca 240
tctggatca tgagtgcctt gaattccttg ctacaaagct taatagtact gcggctttcc 300
ttctgcacag atttggaat cccccacttt ttctgtgaac ttaatcaggt caccacctt 360
gcctgttctg acacctttct taacgacatg gtgatgtatt tgtcatctgc gttgtggggc 420
gggtgctccc tcaactggat cctttactct tactctaaga ttgtttcctc catacgtgca 480
atctcatcag ctcaggggaa gtacaaggca tttccacact atgcgtctca cctctcagtt 540
gtctccttat tttatggtac actcctaggg gtgtacctta gttctgctgc aaccacaac 600
tcatactcaa gtgctgcagc ctgggtgatg tacactgtgg tcaccccc 648

<210> 119

<211> 660

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(660)

<223> Taxon = 9600; gene = PPY52; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127891

<400> 119

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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgagcgg tttgtagccc 180
tctgtcacc cttatatacgt tcagccatct tgaacccgtg tttctgtggc ttcctagatt 240
tgtgggtcttt gttttctttt tcctcagtct tttagactcc cagctgcgca acttgattgc 300
cttacgcatg acctgcttca aggatgtgga aattcctaata tttctctggg aaccttctca 360
actcccccat cttacatttt gtgacacctt caccagtaac atccacatgt atttcctgc 420
tgccgtatatt gggtttcttc ccatctcggg ggcccttttc tcttacggta aaattgtttc 480
ctccattctg aggggtttcat catcagggtg gaagtatcaa ccttctccac ctgtgggtct 540
cacctgtcag ttgtttgctg attttacgga acaggcggtg gagggtagct gggttcagat 600
gtgtcatccc ccccgagaaa ggggtgcagt gcctcagtga tgtacacggt ggtcaccccc 660

<210> 120

<211> 633

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(633) <223> Taxon = 9600; gene = PPY76; pseudogene; Accession
DDBJ/EMBL/ GenBank = AF127892

<400> 120

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acatagcaaa gtcattctcc atgcgggctg tctgacacag atatctttct ttgtcctttt 120
tgcatgtata gatgacatgc tcctgactgt gatggcctat gactgattcg tggccatctg 180
tcacccctg aactaccag tcatcatgaa tcctcacctc tgtgtcttct tagtgttgg 240
gtctttttcc ttagcctgtt ggattcccag ctgcacaatt ggattgttac aattcacctg 300
cttcaagaat gtggaaatct ttaattttgt ctgtgactga tctcaacctt gcctgttctg 360
actgtgtcat cagtaacata ttcatacatt tagatagtac aatacttggg tttcttccca 420
tttcagggat ccttttgtct tactataaaa ttgtgccctc cattctaaga attccattgt 480
cagatgggaa gtataaagcc ttctccacct gtggctctca cctggcaatt gtttgcttat 540
tttatggaac aggcattggg gtgtacctga cttcagctgt gtcactatcc cccaggaatg 600
gtgtgggtcag tgttgtatgt tgtggccacc ccc 633

<210> 121

<211> 648

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 9600; gene = PPY77; pseudogene; Accession DDBJ/EMBL/GenBank = AF127893

<400> 121

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acagaacaaa ttcataacat atgcaggctg tctcggtcag attttctttt tcacttcatt      120
tggatgcctg gacaatttac tcttgaccgt gatggcctat gaccgcttca tggccatctg      180
tcacccctg cactacacac ggtcatcatg aaccaccagc tctgtggact gctggttcta      240
gggtcctagt gcatcagtgt catgggtccc tgctcaagac cttgactgtt ttgaggctgt      300
cctctgcaca aaatggaaat tccacacttt ttttgtgatc ttcttgaagt cctgaagctc      360
gcctgttctg acaccttcat caataacgta gtgatatact ttgcaactgg catcctgggt      420
gtgattccct tcaactggaat acttttctct tactataaaa ttgttttctc tatactgagg      480
atttcctcag ctgggagaaa gtgcaaagcg tttccacct gtggttccca cctctcagt      540
gtcagcttgt tctatggcac aggttttggg gtctatctca gttctgcagc tacaccatct      600
tctaggacaa gtctggtggc ctcaagtgatg tacaccatgg ttaccccc      648
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<210> 122

<211> 660

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(660)

<223> Taxon = 9600; gene = PPY78; pseudogene; Accession DDBJ/EMBL/GenBank = AF127894

<400> 122

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tcacagcaga gtcattctct atgcaggctg cctgactcag atgtgtctcc tggccatttt      120
tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgagcgg tttgtagccc      180
tctgtcacc cctatatcgt tcagccatct tgaaccctg tttctgtggc ttcttagatt      240
tgtggtcttt gttttctttt tctcagctct tttagactcc cagctgcaca acttgattgc      300
cttacgcatg acctgcttca aggatgtgga aattcctaata ttcttctggg aaccttctca      360
actcccccac cttacatttt gtgacacctt caccagtaac atccacatgt atttccctgc      420
```

tgccgtatatt gggtttttctt ccatctcggg ggcccttttc tcttactgta aaactgtttc 480
ctccattctg agggtttcat catcaggtgg ggagtatcaa ccttctccac ctgtgggtct 540
cacctgtcag ttgtttgctt attttatgga acagcccttg gagggtaacct cagttcagct 600
gtgtcccttt cctccaggaa ggggtgcagtg gcctcagtga tgtacctggt ggtcaccccc 660

<210> 123

<211> 649

<212> DNA

<213> Pongo pygmaeus <220> <221> misc_feature

<222> (1)..(649)

<223> Taxon = 9600; gene = PPY85; pseudogene; Accession DDBJ/EMBL/GenBank = AF127855

<400> 123

cttggctgac atcagttttg cctctaccac ggtccccaag atgattgtgg acatccaggc 60
tcacagcaga ctcatctctt atgtgggctg cctgactcag atgtcttttt tgatcctttt 120
cgcatgtatg gaaagtctgc tctgactgt gatggcctat gaccggtttg aggccatctg 180
tcaccccctg cactcccaag tcatcacgag cccacgactc tgtggcctct tagttttggt 240
gtcttttttt cttagccttt tggactctca gctgcacaat ttgattgtgt tacaacttac 300
ctgcttcaat gatgtggaaa tctctaattt tttcctgtga cccttctcaa cttctcagcc 360
tggcctgttc tgacacctcc attaataaca tggctgtata ttttattggt gccatatttg 420
gttttctccc tctcttaggg atccttttct cttactataa aattatttct tccattctgc 480
gagttcgctc ttcaggtggg aagtataaag ccttctccac ctgcagctct cacctgtcag 540
ttgtttgctt attttatgga acagcccttg gagggtaacct cagttcagct gtgtcccttt 600
cctccaggaa ggggtgcagtg gcctcagtga tgtacctggt ggtcacccc 649

<210> 124

<211> 649

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9600; gene = PPY9; Accession DDBJ/EMBL/GenBank = AF127896

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 124

c ttt gta gac atc tgt ttt gcc tct acc acg gtc cca aag atg ctg gtg 49

Phe Val Asp Ile Cys Phe Ala Ser Tnr Tnr Val Pro Lys Met Leu Val				
1	5	10	15	
aat atc cag gca cag agc aaa gtt atc acc tat gca ggc tgc atc acc				97
Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr				
20		25	30	
cag atg tac ttt ttc aca cat ttt gta gga ttg gac agc ttc ctc cta				145
Gln Met Tyr Phe Phe Thr His Phe Val Gly Leu Asp Ser Phe Leu Leu				
35		40	45	
act gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac				193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His				
50		55	60	
tac acg gtc atc atg aac cct caa ctc tgt gga ttg ctg gtt ctg gcg				241
Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala				
65		70	75	80
tcc tgg atc atg agt gtc ttg cat tcc tta tta caa agc tta atg gtg				289
Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val				
85		90	95	
ctg cgg ttg tcc tta tgc aga gag ttg gaa atc ccc cac ttt ttc tgc				337
Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Phe Cys				
100		105	110	
gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac acc ttt ctt gat				385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp				
115		120	125	
gac atg gtg atg tat ttg gca gct gtg ctg ctg ggt ggg gga tgt ctc				433
Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Cys Leu				
130		135	140	
gct ggg atc ctt tac tcc tac tct aag ata gtt tcc tcc ata tgt gca				481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala				
145		150	155	160
atc tca tca gct caa ggg aag tat aag gca ttt tcc acc tgt gca tct				529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser				
165		170	175	
cac ctc tca gtt gtc tcc ttg ttt tat tgt acg agc cta gga gtg tac				577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr				
180		185	190	
ctt agc tcg gct gca atc cac aac tca cac tca agt gca ata gcc tca				625
Leu Ser Ser Ala Ala Ile His Asn Ser His Ser Ser Ala Ile Ala Ser				
195		200	205	
gtg atg tac acc gtg gtc acc ccc				649
Val Met Tyr Thr Val Val Thr Pro				
210		215		

<210> 125
<211> 216
<212> PRT
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY9; Accession DDBJ/EMBL/GenBank = AF127896
<400> 125
Phe Val Asp Ile Cys Phe Ala Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
20 25 30

Gln Met Tyr Phe Phe Thr His Phe Val Gly Leu Asp Ser Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val
85 90 95

Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp
115 120 125

Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Cys Leu
130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Ile His Asn Ser His Ser Ser Ala Ile Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 126
 <211> 649
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 27679; gene = SBO27; Accession DDBJ/EMBL/GenBank = AF127897
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 126

c ctg gtt gat ttc tgt ctg gcc acc gac acc atc ccc aag atg ctg gtg 49
 Leu Val Asp Phe Cys Leu Ala Thr Asp Thr Ile Pro Lys Met Leu Val
 1 5 10 15

agc ctt caa acc agg agc aag gcc atc tct tat ccc tgc tgc ctg acc 97
 Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
 20 25 30

cag atg tac ttc ttc cat ttc ttt ggc atc gtg gac agc gtc tta att 145
 Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Val Leu Ile
 35 40 45

gct gta atg gcg tat gac cgc ttt gtg gcc atc tgc cac ccc ttg cac 193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac gcc acg atc atg agc cca cgc ctc tgt ggc ctg ctg gtc ggg gcc 241
 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala
 65 70 75 80

ccc tgg gtg ttt tca tgc ttc atc tca ctc acc cac atc ctc ctg atg 289
 Pro Trp Val Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
 85 90 95

gcc cgc ctc gtt ttc tgc ggc agc ctc aag gtg cct cat tac ttg tgc 337
 Ala Arg Leu Val Phe Cys Gly Ser Leu Lys Val Pro His Tyr Leu Cys
 100 105 110

gac ctc act ccc atc ctc cga ctt tcg tgc aca gac acg tct gtg aac 385
 Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
 115 120 125

agg att ttc atc ctc act gtg gca ggg atg gtg ata gcc acg ccc ttc 433
 Arg Ile Phe Ile Leu Thr Val Ala Gly Met Val Ile Ala Thr Pro Phe
 130 135 140

atc tgc atc ctg gcc tcc tat gct tgc atc ctt gta gcc atc atg aag 481
 Ile Cys Ile Leu Ala Ser Tyr Ala Cys Ile Leu Val Ala Ile Met Lys
 145 150 155 160

atc ccc tct gca ggt ggc agg aag aaa gcc ttc tcc acc tgc agc tcc 529
 Ile Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175

cac ctg tcc gtg gtt gct ctc ttc tat ggg acc acc att ggg gtc tac 577
 His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
 180 185 190

ctg tgt ccc tcc tcg gtc cac acc gct gta aag gag aaa gct tct gct 625
 Leu Cys Pro Ser Ser Val His Thr Ala Val Lys Glu Lys Ala Ser Ala
 195 200 205

gtg atg tac aca gta gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 127

<211> 216

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO27; Accession DDBJ/EMBL/GenBank = AF127897

<400> 127

Leu Val Asp Phe Cys Leu Ala Thr Asp Thr Ile Pro Lys Met Leu Val
 1 5 10 15

Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Val Leu Ile
 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala
65 70 75 80

Pro Trp Val Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
85 90 95

Ala Arg Leu Val Phe Cys Gly Ser Leu Lys Val Pro His Tyr Leu Cys
100 105 110

Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
115 120 125

Arg Ile Phe Ile Leu Thr Val Ala Gly Met Val Ile Ala Thr Pro Phe
130 135 140

Ile Cys Ile Leu Ala Ser Tyr Ala Cys Ile Leu Val Ala Ile Met Lys
145 150 155 160

Ile Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180 185 190

Leu Cys Pro Ser Ser Val His Thr Ala Val Lys Glu Lys Ala Ser Ala
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 128

<211> 646

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 27679; gene = SBO28; Accession DDBJ/EMBL/GenBank = AF127898

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor

<400> 128

c ttg gct gac att ggt ttc acc tcc acc aca gtc ccc agg aca att gtg 49

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
 1 5 10 15

aac att caa act cac agc aga gtc atc gcc tat gcg agc tgc ctg aca 97
 Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
 20 25 30

cag atg tct ttt tca ata ttt ttt gcg tgt atg gaa gac acg ctc ctg 145
 Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
 35 40 45

gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac 193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg 241
 Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
 65 70 75 80

tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc 289
 Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
 85 90 95

tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt 337
 Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
 100 105 110

gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat 385
 Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
 115 120 125

aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc 433
 Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
 130 135 140

tca ggg atc ttt ttc tct tac tat aaa att gcc ccc tcc att ctg aga 481
 Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Pro Ser Ile Leu Arg
 145 150 155 160

gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct 529
 Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175

cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc att gga gtg tac 577
 His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
 180 185 190

ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg 625
 Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
 195 200 205

atg tac aca gtg gtc act ccc 646
 Met Tyr Thr Val Val Thr Pro
 210 215

<210> 129
<211> 215
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 27679; gene = SBO28; Accession DDBJ/EMBL/GenBank = AF127898
<400> 129

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1 5 10 15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20 25 30

Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Pro Ser Ile Leu Arg
145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
 195 200 205

Met Tyr Thr Val Val Thr Pro
 210 215

<210> 130

<211> 649

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO29; Accession DDBJ/EMBL/GenBank = AF127899

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 130

c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg 289
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
 85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cgc ttt ttc tgc 337
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
 100 105 110

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50 55 60

138

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Ala Leu
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 132

<211> 649

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 132

c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49

Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val															
1				5					10					15	
aat atc cag aca cac agc aaa gtc atc acc ttt gca gac tgc atc acc															97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr															
				20					25					30	
cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg															145
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu															
				35					40					45	
act gtg atg gcc tat gac cgg tat gtg gcc acc tgt cac ccc ctg cac															193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His															
				50					55					60	
tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca															241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala															
				65					70					75	80
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg															289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val															
				85					90					95	
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc															337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys															
				100					105					110	
gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat															385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn															
				115					120					125	
gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc															433
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu															
				130					135					140	
aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca															481
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala															
				145					150					155	160
atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct															529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser															
				165					170					175	
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac															577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr															
				180					185					190	
ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg															625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu															
				195					200					205	
gtg atg tac aca gtg gtc acc ccc															649
Val Met Tyr Thr Val Val Thr Pro															
				210					215						

<210> 133
<211> 216
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900
<400> 133

Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
20 25 30

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His
50 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 134

<211> 649

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 134

c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg 289
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
 85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat 385
 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
 115 120 125

 gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433
 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
 130 135 140

 aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481
 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

 atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

 cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

 ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg 625
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205

 gtg atg cac aca gtg gtc acc ccc 649
 Val Met His Thr Val Val Thr Pro
 210 215

<210> 135

<211> 216

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901

<400> 135

Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

143

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
195 200 205

Val Met His Thr Val Val Thr Pro
210 215

<210> 136

<211> 646

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor

<400> 136

c ttg gct gac att ggt ttc acc tcc acc aca gtc ccc agg aca att gtg 49

<210> 137
<211> 215
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902
<400> 137

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1 5 10 15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20 25 30

Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg
145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
 195 200 205

Met Tyr Thr Val Val Thr Pro
 210 215

<210> 138
 <211> 649
 <212> DNA
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9521; gene = SSC33; Accession DDBJ/EMBL/GenBank = AF127903
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor
 <400> 138
 c ttc tct gac ctc tgc ttc tct tct gtg acc att cca aag ttg tta cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 aac atg cag agc caa gac cca tcc atc ccc tat gcg ggc tgc ctg acc 97
 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
 20 25 30
 cag atg tac ttc ttc ttg tat ttt tgc gat cta gag agc ttc ctc ctt 145
 Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 gtg gcc atg gcc tat gac cgc tac gtg gcc atc tgc ctc ccc cta cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
 50 55 60
 tac gcc acc atc atg agc ccc atg ctg tct cgc tcc ctg gtg gcg ctg 241
 Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
 65 70 75 80
 tcc tgg gtg ctg acc acc ttc cat gcc atg ttg cac act tta ctc atg 289
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95
 gcc agg ttg cgt ttt tgt gca gac aat gtg atc ctc cac ttt ttc tgt 337
 Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
 100 105 110

gat atg tct gct ctg ctg aag ctg gcc tgc tct gac act cga gtt aat 385
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
115 120 125

gaa ttg gtg ata ttt atc atg gga ggc ctc att ctt gtc atc cca ctt 433
Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
130 135 140

cta ctt atc att ggg tcc tac gca cga att gtc ttc tcc atc ctc aag 481
Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys
145 150 155 160

gtc cct tct tct aag ggt atc tgc aag gcc gtc tct act tgt ggc tcc 529
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
165 170 175

cac ctc tct gtg gtg tca ctg ttc tat ggg act gtt att ggt ctc tac 577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
180 185 190

tta tgc cca tca gct aat aat tct act cta aag gag act gtc atg gct 625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
195 200 205

gtg atg tac act gtg atg gcc ccc 649
Val Met Tyr Thr Val Met Ala Pro
210 215

<210> 139

<211> 216

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9521; gene = SSC33; Accession DDBJ/EMBL/GenBank = AF127903

<400> 139

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
50 55 60

Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
65 70 75 80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
85 90 95

Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
115 120 125

Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
130 135 140

Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
195 200 205

Val Met Tyr Thr Val Met Ala Pro
210 215

<210> 140

<211> 646

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 9521; gene = SSC34; Accession DDBJ/EMBL/GenBank = AF127904

<220>

<221> CDS

<222> (2)..(646)

<223> Product =olfactory receptor

<400> 140

c ttg gct gac att ggt ttc acc tcc acc aca gtc ccc agg aca att gtg

<210> 141
<211> 215
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 9521; gene = SSC34; Accession DDBJ/EMBL/GenBank = AF127904
<400> 141

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1 5 10 15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20 25 30

Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg
145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
 195 200 205

Met Tyr Thr Val Val Thr Pro
 210 215

<210> 142
 <211> 649
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 27679; gene = SBO64; pseudogene; Accession DDBJ/EMBL/GenBank = AF127905
 <400> 142

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ctttgtcgat ttctgttatt ccaccaccgt tatacccaaa ctgctggaga acttggttgt      60
ggaagacaga agcatctcct tcacaggatg cgtcatgcaa ttcttttttg ccagcatatt      120
tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tggtggtgtg      180
ttaccctctg ctctacacag ttgcaatgtc ccagaggctt ttctttttgt tagtggctac      240
atcatacttc agggtgacag tctgtttctt gacaattacc ttctttctcc tggaattatc      300
cttcagagga aataatatca ttaataactt tgtgtgtgag cctgctgcca ttgttgctgt      360
gccatgcttt gacccttaca tgagccagga aatcattttc atttctgcca cattcaatga      420
aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat      480
gatgccttcc actggggggc gcataaaagc atgcgcgacc tgttctctcc agctgaccgc      540
cattatcatt ttccatggga ccattctttt tctctattgt gttcctaact ccaaagttc      600
atggctcatg gtcaagggtg gctctatctt ttacacagtg gtcacccc      649

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<210> 143
 <211> 649
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906

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<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 143
c ttt gta gac atc tgt gtt acc tcc acc acg att cca aag aca cta tca      49
  Phe Val Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Thr Leu Ser
    1             5             10             15

aac atc cag aca cac agc aaa gtc atc acc tat gca ggc tgt gtc acc      97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
      20             25             30

cag ttg tac ttt tct gta ctc ttt ata ggg ttg gac agc tta ctc ctg      145
Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu
      35             40             45

acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctg cgc      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
      50             55             60

tac atg gtc atc atg aac cct cag ctc tgt gga ctg ctg gtt ctg gtg      241
Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val
      65             70             75             80

tcc tgg atc atg agt gcc ctg cat tcc ttg aca gaa agc tta atg gca      289
Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala
      85             90             95

tta tca ctg ctc ttt tgt aca gac ttg aaa atc ctc cac ttt ttc tgt      337
Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Phe Cys
      100            105            110

gaa ctt aat cag ata atc cac att gcc tgt tct gac acc tgt ctt aat      385
Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn
      115            120            125

aac ctg gtg atg tat ttg tca gct gtg ctg ctg ggc ggt ggt cct ctc      433
Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu
      130            135            140

gct ggg atc ctg tac tct tac tct aag ata gct tcc tct ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
      145            150            155            160

atc tca tca gct aag ggg aag tac aag gca ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165            170            175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc cta ggg gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
      180            185            190

ctg agt tct gct gca acc cac aac tca ctc tca agt aca gca gcc tcg      625

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Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser
195 200 205

gtg atg tac act gtg gtc acc ccc 649
Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 144
<211> 216
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906
<400> 144

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Thr Leu Ser
1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
20 25 30

Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
50 55 60

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala
85 90 95

Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn
115 120 125

Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu
130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala

[illegible]

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<210> 145
<211> 649
<212> DNA
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor
<400> 145
c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta      49
  Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
    1             5             10             15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc      97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
      20             25             30

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg      145
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
      35             40             45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50             55             60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca      241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65             70             75             80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg      289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val

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155

85	90	95	
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc			337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys			
100	105	110	
gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat			385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn			
115	120	125	
gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc			433
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu			
130	135	140	
aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca			481
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala			
145	150	155	160
atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct			529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser			
165	170	175	
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gcg tac			577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr			
180	185	190	
ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg			625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu			
195	200	205	
gtg atg tac act gtg gtc acc ccc			649
Val Met Tyr Thr Val Val Thr Pro			
210	215		

<210> 146

<211> 216

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907

<400> 146

Phe	Val	Asp	Ile	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Val
1				5						10				15	

Asn	Ile	Gln	Thr	His	Ser	Lys	Val	Ile	Thr	Phe	Ala	Gly	Cys	Ile	Thr
		20						25					30		

Gln	Ile	Gly	His	Cys	Leu	Leu	Phe	Ala	Ala	Leu	Asp	Ile	Phe	Met	Leu
		35					40					45			

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His .
 50 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
 115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
 130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 147
 <211> 487
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(487)

<223> Taxon = 9557; gene = PPA133; Accession DDBJ/EMBL/GenBank = AF179716

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 147

t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1 5 10 15

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35 40 45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga 241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
85 90 95

cgg att gtc tcc tcc atc ctc aag gtc cct tgc tct aag ggt atc tgc 337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc 385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct 433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
130 135 140

act cta aag gag act gtt atg gct atg atg tac act gtg gtg acc ccc 481
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
145 150 155 160

atg ctg 487
Met Leu

<210> 148

<211> 162

<212> PRT

<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA133; Accession DDBJ/EMBL/GenBank = AF179716
<400> 148
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1 5 10 15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
130 135 140

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 149
<211> 486
<212> DNA
<213> Papio hamadryas

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<220>
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<222> (1)..(486)
<223> Taxon = 9557; gene = PPA134; Accession DDBJ/EMBL/GenBank = AF179717
<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor
<400> 149
t gtt gcc atc tgc cag cct ctg cac tac tct acc ctc ttg agc cca tgg      49
  Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
    1             5             10             15

gcc tgc atg gcc atg gtg ggc acc tcc tgg ctc aca ggc atc atc acg      97
Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
    20             25             30

gcc acc acc cat gcc ttc ctc atc ttc tct cta cct ttt ccc agc cgc      145
Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
    35             40             45

cca atc atc cca cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg      193
Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
    50             55             60

gca agt gct ggg aag cac agg agc gag atc tct gtg atg aca gcc act      241
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
    65             70             75             80

gta gtc ttc att atg atc ccc ttc tct ctg att gtc acc tct tac atc      289
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
    85             90             95

cgc atc ctg gga gcc atc cta gcg atg gcc tcc acc cag agc cgc cgc      337
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
    100            105            110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc      385
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
    115            120            125

ttt gga aca gcc agc atc acc tac atc cgg ccg cag gca ggc tcc tct      433
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
    130            135            140

gtt acc aca gac cgc gtc ctc agt gtg ttc tac acg gtc atc aca ccc      481
Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
    145            150            155            160

atg ct      486
Met

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<210> 150
<211> 161
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9557; gene = PPA134; Accession DDBJ/EMBL/GenBank = AF179717
<400> 150

Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
1 5 10 15

Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
20 25 30

Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
35 40 45

Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
50 55 60

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
65 70 75 80

Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
85 90 95

Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
100 105 110

Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
115 120 125

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
130 135 140

Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
145 150 155 160

Met

<210> 151

<211> 487
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA135; pseudogene; Accession DDBJ/EMBL/Genbank = 179718
<400> 151
tgtggacatc tgaagtcctt tgcactaccc agtcatcatg aacgaaagaa cacggggccaa 60
actggctgct gcttcctggt tcccaggctt tcctgtagct actgtgcaga ccacgtggct 120
cttcagcttt ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccacc 180
tgtgtgaag ctggctctgtg tagacacagc actgtttgag atctacacca tctactggaac 240
cattctgggtg gtcatgatcc cctgcttgcg gatcttctgt tcctacactc tcattgctgc 300
tgccatcctc aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgatcctc 360
acatctcctt gttgtctctc ttttctatct atcattaaac ctcacatatt ttcagcctaa 420
atcaaataat tctcctgaaa gcaaaaagct gctatcattg ttctacactg ttgtgactcc 480
catgttg 487

<210> 152
<211> 482
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(482)
<223> Taxon = 9557; gene = PPA136; pseudogene; Accession DDBJ/EMBL/Genbank = 179719
<400> 152
tgtggccatc tgccaccccc tctactatgt cacagccatg agtcctggac tctgtatctt 60
gctcctctgc ttgtgttggg ggctctctgt tctctatggt ctctcctca ctctcctct 120
gaccaggggtg accttctgtg ggactcaaga gatccactac ctcttctgtg agatgtacgt 180
cctgctgcag ctggcatggt ccaacaccca catcattcac acagtgctgg ttgctactgg 240
ctgctttctt cctcgacccc ttaggggttca cgactacatc ctatatacgt attgtcagaa 300
ccatccttca gataacctca gcctctaaga aacacaaaac cttctctgcc tgtgcctcac 360
atgtgggtgt ggtctccctc ttttatggga cacttggtat ggtatacctg cagccccctc 420
acacctactc catgaaggac tcagtagcca cagtgatgta tgctgtgggtg acacctatga 480

tg

482

<210> 153
 <211> 481
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(481)
 <223> Taxon = 9557; gene = PPA137; Accession DDBJ/EMBL/GenBank = AF179720
 <220>
 <221> CDS <222> (2)..(481)
 <223> Product = olfactory receptor
 <400> 153
 c ctg gca ata tgt caa ccc ctg cgc tac cca gtg ctc atg aat ggg agg 49
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
 1 5 10 15

 tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat 97
 Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
 20 25 30

 ggg tct atc cag gcc acc ctg acc ttc cgc cta ccc tat tgt ggg ccc 145
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
 35 40 45

 aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg 193
 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
 50 55 60

 gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc 241
 Ala Cys Ala Asp Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
 65 70 75 80

 gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat gcc 289
 Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
 85 90 95

 aac ata gtc cat gcc atc ctg aag ata cgc acc act gat ggg agg cgc 337
 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
 100 105 110

 cgg gcc ttc tct acc tgt ggc tcc cac cta act gtg gtc aca gtc tac 385
 Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr
 115 120 125

 tat gtt ccc tgt att ttc atc tac ctt agg gct ggc tcc aag agc ccc 433
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro
 130 135 140

 ctg gat ggg gca gtg gct gtg ttt tac act gtt gtc act cca ttc ctg 481
 Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu
 145 150 155 160

<210> 154
<211> 160
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(481)
<223> Taxon = 9557; gene = PPA137; Accession DDBJ/EMBL/GenBank = AF179720
<400> 154

Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
1 5 10 15

Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
20 25 30

Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
35 40 45

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
50 55 60

Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
65 70 75 80

Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
85 90 95

Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
100 105 110

Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr
115 120 125

Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro
130 135 140

Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu
145 150 155 160

<210> 155
<211> 487
<212> DNA

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<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA138; Accession DDBJ/EMBL/GenBank = AF179721
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 155
t gta gcc ata tgc aaa cct tta ctt tat cca gtg att atg acc aat gga      49
  Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly
    1             5             10             15

ctg tgc atc cgg cta tta gtc ttg tca ttt gta ggt ggc ttc ctt cat      97
Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
      20             25             30

gcc tta att cat gaa ggc att tta ttc aga tta acc ttc tgt aat tct      145
Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
      35             40             45

aac ata ata cat cac ttt tac tgt gac att atc cca ttg tta acg att      193
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
      50             55             60

tcc tgt act gac cct tct att aat ttt tta atg ctt ttt att ttg tct      241
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
      65             70             75             80

ggt tca ata cag gta ttc act att ttg act gtt ctt gtc tct tat gca      289
Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
      85             90             95

ttt gtc ctc ttt aca atc tta aaa aaa aag tca gtc aaa ggc ata agg      337
Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg
      100            105            110

aaa gcc ttt tcc acc tgt gga gcc cat ctc ttc tct gtc tgt tta tac      385
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
      115            120            125

tat ggc ccc ctt ctc ttc atg tat gtg ggc cct gca tct cca caa gca      433
Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
      130            135            140

gat gat caa gat atg gta gag tgt gta ttt tac act gtc atc att cct      481
Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
      145            150            155            160

ttc tta
Phe Leu
      487

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<210> 156
<211> 162
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA138; Accession DDBJ/EMBL/GenBank = AF179721
<400> 156

Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly
1 5 10 15

Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
20 25 30

Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
35 40 45

Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
50 55 60

Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
65 70 75 80

Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
85 90 95

Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
115 120 125

Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
130 135 140

Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
145 150 155 160

Phe Leu

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<210> 157
<211> 487
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 157
t gtg gcc att tgt aac cct ctg ctc tac atg gtg gtg gtg tct cgg cgg      49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
    1             5             10             15

ctc tgc ctc ctg ctg gtc tcc ctc aca tac ctc tat ggc ttt tct aca      97
Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
      20             25             30

gct att gtg gtt tca cct tgt ata ttc tct atg tct tat tgc tct tct      145
Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
      35             40             45

aat ata atc aat cat ttt tac tgt gat att gca cct ctg tta gca tta      193
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
      50             55             60

tct tgc tct gat act tac tta cca gaa gca ata gtc ttc ata tct gca      241
Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
      65             70             75             80

gca aca aat ttg gtt ttt tcc atg att aca gtt cta gta tct tat ttc      289
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
      85             90             95

aat att gtt ttg tcc att cta agg atg cat tca tca gaa gga agg aaa      337
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
      100            105            110

aaa gcc ttt tcc acc tgt gct tca cat atg atg gca gtc aca gtt ttc      385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
      115            120            125

tat ggg aca atg ctg ttc atg tat ttg cag ccc caa acc aac cac tca      433
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
      130            135            140

ctg gat act gat aag atg gct tct gtg ttt tac aca ttg gtg att cct      481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
      145            150            155            160

atg ctg      487

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Met Leu

<210> 158
<211> 162
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722
<400> 158

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
1 5 10 15

Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
20 25 30

Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
35 40 45

Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
50 55 60

Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
65 70 75 80

Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
85 90 95

Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
115 120 125

Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
145 150 155 160

Met Leu

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<210> 159
<211> 487
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF179723
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 159
t  gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
   Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
     1             5             10             15

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
   Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
     20             25             30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgc gca gac      145
   Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
     35             40             45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
   Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
     50             55             60

gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga      241
   Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
     65             70             75             80

ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
   Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
     85             90             95

cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc      337
   Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
    100             105             110

aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc      385
   Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
    115             120             125

tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct      433
   Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
    130             135             140

act cta aag gag act gtt atg ggt atg atg tac act gtg gtg acc ccc      481
   Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro

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145

150

155

160

atg ctg

487

Met Leu

<210> 160

<211> 162

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF179723

<400> 160

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1 5 10 15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
130 135 140

Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

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<210> 161
<211> 478
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(478)
<223> Taxon = 9557; gene = PPA142; Accession DDBJ/EMBL/GenBank = AF179724
<220>
<221> CDS
<222> (2)..(478)
<223> Product = olfactory receptor
<400> 161
t  gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct      49
   Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro
     1              5              10              15

atg  tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat      97
   Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
     20              25              30

gga ggg atc cag act ctg ttc ata gcc cag tta cca ttc tgt ggc ccc      145
   Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
     35              40              45

aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg      193
   Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
     50              55              60

gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt      241
   Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
     65              70              75              80

gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc      289
   Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
     85              90              95

atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa      337
   Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
    100              105              110

gct ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt      385
   Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
    115              120              125

gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ccc act      433
   Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
    130              135              140

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gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg 478
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145 150 155

<210> 162

<211> 159

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(478)

<223> Taxon = 9557; gene = PPA142; Accession DDBJ/EMBL/GenBank = AF179724

<400> 162

Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro
1 5 10 15

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
20 25 30

Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
35 40 45

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
50 55 60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
65 70 75 80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
85 90 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
100 105 110

Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
115 120 125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
130 135 140

Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145 150 155

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<210> 163
<211> 487
<212> DNA
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA143; Accession DDBJ/EMBL/GenBank = AF179725
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 163
t gtg gcc atc tgc aag cct ctg cat tac ttg aat atc atg aat cga aga      49
Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
  1              5              10              15

gtc tgc aca ctg ctt gtt ttt act tct tgg ctg gtt tca ttc tta atc      97
Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
      20              25              30

ata ttc cca gca ctc atg ttg ctc tta cag ctt gat tac tgt agg tct      145
Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
      35              40              45

aat att atg gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt      193
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
      50              55              60

gct tgt tca gac aca aaa ttc cta gag gtg atg gga ttt tct tgt gct      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
      65              70              75              80

gtg ttt act cta atg ttg act ttg gca tta ata ttt ctg tcc tac ata      289
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
      85              90              95

tac att atc aga aca att ttg aga att cct tct gct agt caa agg aca      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
      100              105              110

aag gcc ttt tcc aca tgt tct tcc cac atg att gtc atc tcc atc tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
      115              120              125

tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
      130              135              140

gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc      481
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
      145              150              155              160

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atg ctg
Met Leu

487

<210> 164
<211> 162
<212> PRT
<213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA143; Accession DDBJ/EMBL/GenBank = AF179725
<400> 164

Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
1 5 10 15

Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
20 25 30

Ile Phe Pro Ala Leu Met Leu Leu Gln Leu Asp Tyr Cys Arg Ser
35 40 45

Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
65 70 75 80

Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Met Leu

```

<210> 165
<211> 487
<212> DNA <213> Papio hamadryas
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA144; Accession DDBJ/EMBL/GenBank = AF179726
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 165
t gtt gcc atc tgc cag cct ctg cac tac tct acc ctc ttg agc cca tgg      49
Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
1          5          10          15

gcc tgc atg gcc atg gtg ggc acc tcc tgg ctc aca ggc atc atc acg      97
Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
20          25          30

gcc acc acc cat gcc ttc ctc atc ttc tct cta cct ttt ccc agc cgc      145
Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
35          40          45

cca atc atc cca cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg      193
Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
50          55          60

gca agt gct ggg aag cac agg agc gag atc tct gtg atg aca gcc act      241
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
65          70          75          80

gta gtc ttc att atg atc ccc ttc tct ctg att gtc acc tct tac atc      289
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
85          90          95

cgc atc ctg gga gcc atc cta gcg atg gcc tcc acc cag agc cgc cgc      337
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
100         105         110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc      385
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
115         120         125

ttt gga aca gcc agc atc acc tac atc cgg ccg cag gca ggc tcc tct      433
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
130         135         140

gtt acc aca gac cgc gtc ctc agt ctc ttc tac acg gtc atc aca ccc      481
Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro

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145

150

155

160

atg ctc

487

Met Leu

<210> 166

<211> 162

<212> PRT

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(487) <223> Taxon = 9557; gene = PPA144; Accession
DDBJ/EMBL/GenBank = AF179726

<400> 166

Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
1 5 10 15Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
20 25 30Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
35 40 45Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
50 55 60Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
65 70 75 80Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
85 90 95Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
100 105 110Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
115 120 125Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
130 135 140Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
145 150 155 160

Met Leu

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<210> 167
<211> 487
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR183; Accession DDBJ/EMBL/GenBank = AF179727
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 167
t  gtg gcc atc tgt ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
   Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
   1              5              10              15

ctc tgt ctc tcc gtg gtg acg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His
      20              25              30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
      35              40              45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
      50              55              60

gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
      65              70              75              80

ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
      85              90              95

aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
      100             105             110

aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
      115             120             125

tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
      130             135             140

```


act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 168

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR183; Accession DDBJ/EMBL/GenBank = AF179727

<400> 168

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 169
 <211> 487
 <212> DNA
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 169
 t gtg gcc atc tgt ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15
 ctc tgt ctc tcc gtg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97
 Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30
 gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145
 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45
 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg 193
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60
 gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga 241
 Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80
 ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289
 Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95
 aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc 337
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110
 aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc 385
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct 433
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
 130 135 140

act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 170
 <211> 162
 <212> PRT
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728
 <400> 170
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 171
<211> 485
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 9598; gene = PTR204; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179729

<400> 171
tgtagccata tgtaatccct tgctttatcc agtgatgatg tccaacaaac tcagcgctca 60
gttgctaagc atttcatatg taattgggtt cctgcaccc ctgggttcacg tgagtttact 120
attgcgacta actttctgca ggtttaacat aatacattat ttctactgtg aaattttaca 180
actgttcaaa atttcatgca atgggtccatc tattaacgca ctaatgatat ttatttttgg 240
tgcttttata caaataccca ctttaatgac gatcataatc tcttatactc gtgtgctctt 300
tgatattctg aaaaaaaagt ctgaaaaggc cagaagcaaa gccttctcca catgcagcgc 360
ccatctgctt tctgtctcat tgtactacgg aactctgac ttcatgtatg tgcgtcctgc 420
atctggctta gctgaagacc cagacaaagt gtattctctt ttacacgatt ataattcccc 480
tgcta 485

<210> 172
<211> 487
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR205; Accession DDBJ/EMBL/GenBank = AF179730
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 172

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t gtg gcc att tgc cgc ccc ctc tgc tac tcc aca gtc acg agg ccc caa      49
Val Ala Ile Cys Arg Pro Leu Cys Tyr Ser Thr Val Thr Arg Pro Gln
1          5          10          15

gtc tgt gcc cta atg ctt gca ttg tgc tgg gtc ctc acc aat atc att      97
Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
20          25          30

gcc ctg act cac acg ttc ctc atg gct cgg ttg tcc ttc tgt gtg act      145
Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
35          40          45

ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag ctg      193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
50          55          60

tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga      241
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
65          70          75          80

ggc acc gta ctc atc gtc ccc ttt tta tgc att gtc acc tcc tac atc      289
Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
85          90          95

cac att gtg cca gct atc ctg agg gtc cga acc cgt ggt ggg gtg ggc      337
His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly
100          105          110

aag gcc ttt tcc acc tgc agt tcc cac ctc tgc gtt gtt tgt gtg ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe
115          120          125

tat ggg acg ctc ttc agt gcc tac ctg tgt cct ccc tcc att gcc tct      433
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130          135          140

gaa gag aag gac att gca gca gct gca atg tac acc ata gtg act ccc      481
Glu Glu Lys Asp Ile Ala Ala Ala Ala Met Tyr Thr Ile Val Thr Pro
145          150          155          160

atg ttg      487
Met Leu

```

<210> 173

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR205; Accession DDBJ/EMBL/GenBank = AF179730

<400> 173

Val Ala Ile Cys Arg Pro Leu Cys Tyr Ser Thr Val Thr Arg Pro Gln
1 5 10 15

Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
20 25 30

Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
35 40 45

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
65 70 75 80

Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
85 90 95

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe
115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130 135 140

Glu Glu Lys Asp Ile Ala Ala Ala Ala Met Tyr Thr Ile Val Thr Pro
145 150 155 160

Met Leu

<210> 174

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR206; Accession DDBJ/EMBL/GenBank = AF179731

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 174

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c gtg gcc atc tgt cac cct tta cat tac tcc acc att atg gcc ctg cgc      49
  Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
    1             5             10            15

ctc tgt gcc tct ctg gta gct gca cct tgg gtc att gcc att ttg aac      97
Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn
      20             25            30

cct ctc ttg cac act ctt atg atg gcc cat ctg cac ttc tgc tct gat      145
Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp
      35             40            45

aat gtt atc cac cat ttc ttc tgt gat atc aac tct ctc ctc cct ctg      193
Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu
    50             55            60

tcc tgt tcc aac acc agt ctt aat cag ttg agt gtt ctg gct acg gtg      241
Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val
    65             70            75            80

ggg ctg atc ttt gtg gta cct tca gtg tgt atc ctg gta tcc tat atc      289
Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile
      85             90            95

ctc att gtt tct gct gtg atg aaa gtc cct tct gcc caa gga aaa ctc      337
Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu
      100            105           110

aag gct ttc tct atc tgt gga tct cac ctt gcc ttg gtc att ctt ttc      385
Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe
      115            120           125

tat gga gca atc aca ggg gtc tat atg agc ccc tta tcc aat cac tct      433
Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser
      130            135           140

act gaa aaa gac tca gcc gca tca gtc att ttt atg gtt gta gca cct      481
Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro
      145            150           155           160

gtg ttg      487
Val Leu

```

<210> 175

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR206; Accession DDBJ/EMBL/GenBank = AF179731

<400> 175

Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
1 5 10 15

Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn
20 25 30

Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp
35 40 45

Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu
50 55 60

Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val
65 70 75 80

Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile
85 90 95

Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu
100 105 110

Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe
115 120 125

Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser
130 135 140

Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro
145 150 155 160

Val Leu

<210> 176

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 176

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t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tac cag agg      49
Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
  1              5              10              15

ctt tgc tcc ttg ttg gtg gct aca tca tac tgt tgg ggg aga gtc tgt      97
Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
      20              25              30

tcc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat      145
Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
      35              40              45

aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg      193
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
      50              55              60

tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc      241
Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
      65              70              75              80

aca ttc aat gaa ata agc agc ctg gtg atc act ctc act tcc tat gct      289
Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
      85              90              95

ttc att ttt atc act gtc atg aag acg gct tcc att ggg ggg cgc aag      337
Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
      100              105              110

aaa gcg ttc ttc acg tgt gcc tcc cac ttg acg gcc att acc att ttc      385
Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
      115              120              125

cat ggg act att ctt ttc ctc tac tgt gtt cct aac tcc aaa agt tcg      433
His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
      130              135              140

tgg ctc atg gtc aag gtg gcc tct gtc ttt tac aca gtg gtc att ccc      481
Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
      145              150              155              160

atg ctg      487
Met Leu

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<210> 177

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732

<400> 177

Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
1 5 10 15

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
20 25 30

Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
65 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
85 90 95

Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
100 105 110

Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
115 120 125

His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
130 135 140

Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
145 150 155 160

Met Leu

<210> 178

<211> 481

<212> DNA

<213> Pan troglodytes

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<220>
<221> misc_feature
<222> (1)..(481)
<223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733
<220>
<221> CDS
<222> (2)..(481)
<223> Product = olfactory receptor
<400> 178
c ctg gca ata tgt cag ccc ctg cgc tac cca gtg ctc atg aat ggg agg      49
  Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
    1             5             10             15

tta tgc aca gtc ctt gtg gct gga gct tgt gtc gcc ggc tcc atg cat      97
  Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His
            20             25             30

ggg tct atc cag gcc acc ctg acc ttc cgc ctg ccc tac tgt ggg ccc      145
  Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
            35             40             45

aat cag gtg gat tac ttt atc tgt gac atc ccc gca gta ttg aga ctg      193
  Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
            50             55             60

gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc      241
  Ala Cys Ala Asp Thr Val Val Asn Glu Leu Val Thr Phe Val Asp Val
        65             70             75             80

ggg gtg gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcg tat gcc      289
  Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
            85             90             95

aac ata gta aat gcc atc ctg aag ata cgc acc act gat ggg agg cac      337
  Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His
            100            105            110

cgg gcc ttc tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac      385
  Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
            115            120            125

tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa ggc ccc      433
  Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
            130            135            140

ctg gat ggg gcg gcg gct gtg ttt tac act gtt gtc act cca tta ctg      481
  Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
        145            150            155            160

<210> 179
<211> 160
<212> PRT
<213> Pan troglodytes

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<220>
<221> misc_feature
<222> (1)..(481)
<223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733
<400> 179
Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
1 5 10 15

Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His
20 25 30

Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
35 40 45

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
50 55 60

Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
65 70 75 80

Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
85 90 95

Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His
100 105 110

Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
115 120 125

Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
130 135 140

Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
145 150 155 160

<210> 180
<211> 487
<212> DNA
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734
<220>

<221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 180
 c gtg gcc atc tgt cac ccc ctg tac tac cgt gtc atc gtg aac ccc cgc 49
 Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg
 1 5 10 15

 ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac 97
 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
 20 25 30

 tcc ctg atc cag agt ctg ttg atg ctg cag gtg tcc ttc tgt acc agt 145
 Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser
 35 40 45

 tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt 193
 Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
 50 55 60

 acc tgc tca gac aca cac gtc aat tac atc ctg ctg tac gtg gtg act 241
 Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr
 65 70 75 80

 ggc ctt ctg gac ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc 289
 Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
 85 90 95

 caa att gtc tcc tac atc cta aga atc tca tcc aca gat ggg aaa cac 337
 Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His
 100 105 110

 aaa gcc ttt tct acc tgt gga tct cat ctg ttt gtg gtt tct tta ttc 385
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe
 115 120 125

 tat ggg aca ggc ctt ggt gtg tat ctt agt tcc aat gca tgc tcc tct 433
 Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
 130 135 140

 tcc tgg tgg ggc atg gtg gcc tgc gtc atg tac act gtg gtc acc ccc 481
 Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

 atg ctg 487
 Met Leu

<210> 181
 <211> 162
 <212> PRT
 <213> Pan troglodytes
 <220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734

<400> 181

Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg
1 5 10 15

Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
20 25 30

Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser
35 40 45

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
50 55 60

Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr
65 70 75 80

Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
85 90 95

Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
130 135 140

Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 182

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

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<222> (1)..(487)
<223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 182
t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa      49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
    1              5              10              15

ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat      97
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
      20              25              30

cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt      145
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
      35              40              45

aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att      193
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
      50              55              60

tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt      241
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
      65              70              75              80

gct ttt ata caa ata ccc act tta atg acg atc ata atc tct tat tct      289
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
      85              90              95

cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc      337
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
      100              105              110

aaa gcc ttc tcc aca tgc agc gcc cat ctg ctt tct gtc tca ttg tac      385
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
      115              120              125

tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct      433
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
      130              135              140

gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc      481
Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
      145              150              155              160

ctg cta
Leu Leu
      487

<210> 183
<211> 162

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<212> PRT
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = .9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735
<400> 183
Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15

Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30

Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45

Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
50 55 60

Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
65 70 75 80

Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
85 90 95

Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
115 120 125

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
130 135 140

Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145 150 155 160

Leu Leu

<210> 184
<211> 487
<212> DNA


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<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 184
t  gtg gcc att tgc cac cca ctg agg tac aca gtc ctc atg aac atc cat      49
   Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
   1              5              10              15

   ttc tgc ggc ttg ctg att ctt ctc tcc agg ttc atg agc act atg gat      97
   Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
           20              25              30

   gcc ctg gtt cag agt ctg atg ata ttt cag ctg tcc ttc tgc aaa aac      145
   Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
           35              40              45

   gtt gaa atc cct ttg ttc ttc tgt gaa gtc gtt cag gtc atc aag ctc      193
   Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
           50              55              60

   gcc tgt tct gac acc ctc atc aac aac atc ctc ata tat ttt gca agt      241
   Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
           65              70              75              80

   agc ata ttt ggt gca att cct ctc tct gga ata att ttc tct tat tct      289
   Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
           85              90              95

   caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga aag tat      337
   Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
           100              105              110

   aaa gcg ttt tcc acc tgt ggc tgt cac ctc tct gtt ttt tcc ttg ttc      385
   Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
           115              120              125

   tat ggg aca gct ttt ggg gtg tcc att agt tct gct gtt gct gag tct      433
   Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
           130              135              140

   tcc cga att act gct gtg ggt tca gtg atg tac act gtg gtc cca caa      481
   Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
           145              150              155              160

   atg atg      487
   Met Met

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<210> 185
<211> 162
<212> PRT
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736
<400> 185

Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
1 5 10 15

Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
20 25 30

Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
35 40 45

Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
50 55 60

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
65 70 75 80

Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
85 90 95

Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
115 120 125

Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
130 135 140

Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
145 150 155 160

Met Met

Met Leu

<210> 187
<211> 162
<212> PRT
<213> Pan troglodytes
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR212; Accession DDBJ/EMBL/GenBank = AF179737
<400> 187
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 188
 <211> 484
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(484)
 <223> Taxon = 9580; gene = HLA121; pseudogene; Accession DDBJ/EMBL/GenBank = AF179738
 <400> 188
 tgtggctatc tgcctgccgc ttaggtatcc agagctcatg agtgggcaga cctgcatgca 60
 gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccacccctgt 120
 ctgggcgctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc 180
 agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tgggtggccac 240
 agctgtcctg acactggccc ccctcttgct catctgcctg tcttaccttt tcatcttgtc 300
 tgccatcctt aggggtaccct ctgctgcagg cgggcgcaaa gccttctcca cctgctcagc 360
 ccacctcaca gtgggtgggtg ttttttaagg gacaatttcc ttcatgtact tcaaacccaa 420
 ggccaaggac cccaacgtgg ataagattgt tgcattgttg tatgggggtg tgacaccctc 480
 gctg 484

<210> 189
 <211> 487
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 189
 t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tcc cag agg 49
 Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
 1 5 10 15
 ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt 97
 Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
 20 25 30
 ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat 145

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Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
   35                               40                               45

aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg      193
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
   50                               55                               60

tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc      241
Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
   65                               70                               75                               80

aca ttc aat gaa ata agc agt ctg atg atg att ttc act tcc tat gct      289
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
                               85                               90                               95

ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag      337
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
                               100                               105                               110

aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc      385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
                               115                               120                               125

cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca      433
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
                               130                               135                               140

tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc      481
Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
   145                               150                               155                               160

atg gtg      487
Met Val

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<210> 190

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

<400> 190

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Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
1                               5                               10                               15

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Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
20                               25                               30

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Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn

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35 40 45
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
 50 55 60
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
 65 70 75 80
 Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
 85 90 95
 Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
 115 120 125
 His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
 130 135 140
 Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
 145 150 155 160
 Met Val

<210> 191
 <211> 486
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740
 <220>
 <221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor
 <400> 191
 t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15
 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

20	25	30	
gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac			145
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp			
35	40	45	
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg			193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu			
50	55	60	
tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga			241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly			
65	70	75	80
ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt			289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly			
85	90	95	
cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc			337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys			
100	105	110	
aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat			385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr			
115	120	125	
tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc			433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr			
130	135	140	
aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc			481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro			
145	150	155	160
atg tt			486
Met			

<210> 192

<211> 161

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740

<400> 192

Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Ser
1				5					10					15	

Gln	Cys	Val	Met	Leu	Val	Ala	Gly	Ser	Trp	Val	Ile	Ala	Cys	Ala	Cys
		20						25					30		

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met

<210> 193

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 193

t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg 49
 Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
 1 5 10 15

```

act cgt gcc aaa ctg gct gct gcc tcc tgg ttc cca ggc ttt cct gta      97
Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
          20                      25                      30

gct act gtg cag acc aca tgg ctc ttc agt ttt cca ttc tgt ggc acc      145
Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
          35                      40                      45

aac aag gta aac cac ttc ttc tgt gac agc ccg cct gtg ctg agg ctg      193
Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu
          50                      55                      60

gtc tgt gca gac aca gca ctg ttt gag atc tac gcc atc gtc gga acc      241
Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
          65                      70                      75                      80

att ctg gtg gtc atg atc cct tgc ttg ctg atc ttg tgt tcc tat act      289
Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
          85                      90                      95

cac att gct gct gcc atc ctc aag atc cca tcg gct aaa ggg aag aat      337
His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn
          100                      105                      110

aaa gcc ttc tct acg tgt tcc tca cac ctc ctt gtt gtc tct ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
          115                      120                      125

tat ata tca tta agc ctc aca tat ttt cgg cct aaa tca aat aat tct      433
Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser
          130                      135                      140

cct gag ggc aag aag ctg cta tca ttg tcc tac act gtt gtg act ccc      481
Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro
          145                      150                      155                      160

atg ttg
Met Leu
487

```

<210> 194

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<400> 194

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Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
1          5          10          15

```

Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
20 25 30

Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
35 40 45

Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu
50 55 60

Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
65 70 75 80

Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
85 90 95

His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
115 120 125

Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser
130 135 140

Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 195

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 195

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t gtg gcc atc tgc aag cct ctg cat tac ttg aat atc atg aat cga aga      49
Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
1           5           10           15

gtc tgc ata ctg ctt gtt ttt act tct tgg ctg att tca ttc tta atc      97
Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
20           25           30

ata ttc cct gca ctc atg ttg ctc tta aag ctt gat tac tgt agg tct      145
Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
35           40           45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt      193
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50           55           60

gct tgt tca gac aca aaa ttc tta gag gtg atg gca ttt tct tgt gct      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
65           70           75           80

gtg ttt act cta atg ttc act ttg gca tta ata tct ctg tcc tac ata      289
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
85           90           95

tac att atc aga aca att ttg aga att cct tct act agt cag agg aca      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
100          105          110

aag gcc ttt tcc aca tgt tct tcc cac atg gtt gtt att tcc atc tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
115          120          125

tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130          135          140

gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc      481
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
145          150          155          160

atg atg      487
Met Met

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<210> 196

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487) <223> Taxon = 9580; gene = HLA125; Accession
DDBJ/EMBL/GenBank = AF179742

<400> 196

Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
1 5 10 15

Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
20 25 30

Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
35 40 45

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
65 70 75 80

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Met Met

<210> 197

<211> 484

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743

<220>

<221> CDS

<222> (2) . . (484)

<223> Product = olfactory receptor

<400> 197

t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag 49
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

ctc tgt gtc ttc tta gtg gct ata tct tgg att ctg tct tgt gcc agc 97
Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg 145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337
 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
 100 105 110

aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat 385
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
115 120 125

ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att 433
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
130 135 140

gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg 481
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145 150 155 160

ttg	484
Leu	

<210> 198

<211> 161

<212> PRT

<213> Hylobates lar

<220>

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<221> misc_feature
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<222> (1)..(484)

<223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743

<400> 198

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145 150 155 160

Leu

<210> 199

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 199

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
35 40 45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg 193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga 241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt 289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc 337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

aaa gcc ttg tcc att tgt gga tcc cac ctc tca gtg gtg act atc tat 385
Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc 433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

atg ttg 487
Met Leu

<210> 200

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744

<400> 200

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 201

<211> 484

<212> DNA

<213> Hylobates lar

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<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank = AF179745
<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor
<400> 201
t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag      49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
    1              5              10              15

ctc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc      97
Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
      20              25              30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35              40              45

aac acc atc ccc cac gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50              55              60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65              70              75              80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85              90              95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100             105             110

aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat      385
Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
      115             120             125

ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att      433
Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
      130             135             140

gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg      481
Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
      145             150             155             160

ttg
Leu
      484

```

<210> 202
<211> 161
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank AF179745
<400> 202
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145 150 155 160

Leu

<210> 203

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<211> 484
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746
<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor
<400> 203
t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc      49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
    1             5             10             15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt      97
  Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
        20             25             30

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac      145
  Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
        35             40             45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg      193
  His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
        50             55             60

tcc tgc tca gat acc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
  Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
        65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
  Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
        85             90             95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
  Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
        100            105            110

aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat      385
  Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
        115            120            125

ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att      433
  Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
        130            135            140

gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg      481
  Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
        145            150            155            160

ttg
Leu

```

<210> 204
<211> 161
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746
<400> 204

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145 150 155 160

Leu

<210> 205
 <211> 486
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9580; gene = HLA130; pseudogene; Accession DDBJ/EMBL/GenBank = AF179747
 <400> 205
 tgtggccatc tgtcaccctc tacattatgc accatcatga gtcagagcca gtgtgtcatg 60
 ctggtggctg ggtcctgggt catcgcttgt gcgtgtgctc ttttgcatc cctcctcctg 120
 gcccagcttt ccttttgtgc tgaccacatc atccctcact tcttctgtga ccttggtgcc 180
 ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga 240
 ttgacagcca ttatgcttcc attcttgtgc atcctgggtt cttatgggtca cattggggtc 300
 accatcctcc agattccctc taccaagggc atatgcaaag ccttgtccat ttgtggatcc 360
 cacctctcag tggtgactat ctattatggg acaattattg gtctctattt tcttccccca 420
 tccagcaaca ccaatgacaa gaacataatt gcttcagtga tatacacagt agtcactccc 480
 atgttg 486

<210> 206
 <211> 487
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA131; Accession DDBJ/EMBL/GenBank = AF179748
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 206
 t gtg gcc atc tgt cgc ccc ctg tac tac cct gtc atc atg aaa cct cac 49
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
 1 5 10 15
 ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac 97
 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
 20 25 30
 tcc ctg atc cag agt ctg ttg atg ctg cgg gtg tcc ttc tgc acc agt 145
 Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser

35	40	45	
tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt			193.
Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu			
50	55	60	
gcc tgc tca gac aca cac atc aat tac atc ctg ctc tac atg gtg acc			241
Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr			
65	70	75	80
ggc ctt ttg ggc ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc			289
Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr			
	85	90	95
caa atc gtc tcc tcc atc ctg aga atc tca tcc cca gat ggg aaa cac			337
Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His			
	100	105	110
aaa gcc ttt tct acc tgt gga tct cat ctg tct gtg gtt tct tta ttc			385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe			
	115	120	125
tat ggg aca ggt ctt ggc gtg tat ctt agt tcc aat gca tcg tcc tct			433
Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser			
	130	135	140
tcc tgg cgg ggc atg gtg gct tcg gta atg tac act gtg gta acc ccc			481
Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro			
145	150	155	160
aat gtg			487
Asn Val			

<210> 207

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA131; Accession DDBJ/EMBL/GenBank = AF179748

<400> 207

Val	Ala	Ile	Cys	Arg	Pro	Leu	Tyr	Tyr	Pro	Val	Ile	Met	Lys	Pro	His
1				5					10				15		

Leu	Cys	Gly	Leu	Leu	Val	Leu	Val	Ser	Trp	Phe	Leu	Ser	Leu	Ser	Tyr
			20					25					30		

Ser	Leu	Ile	Gln	Ser	Leu	Leu	Met	Leu	Arg	Val	Ser	Phe	Cys	Thr	Ser
			35				40					45			

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
 50 55 60

Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
 65 70 75 80

Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
 85 90 95

Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
 130 135 140

Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Asn Val

<210> 208

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA132; Accession DDBJ/EMBL/GenBank = AF179749

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 208

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg.tgt 97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 210

<211> 487

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 210

t gta gcc att tgt cat cct ctt cat tat acc ttc att atg gac caa aac 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
 1 5 10 15

```

acc tgc att caa ctg gca gtt att tct tgg tcc agt agc ttc ctg tgt      97
Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
          20                      25                      30

tcc atg gtt atc aat gtt ctc acg ttg agt ttg ccc tac tgt ggg cct      145
Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
          35                      40                      45

aat atc ctg aat cac ttt ttc tgt gag gta cct act gtc ctg agg ttg      193
Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
          50                      55                      60

tct tgc acc gac acc tca ttc acg gag ctg gtt gtt ttt atc ttc agt      241
Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
        65                      70                      75                      80

atc atc att gtc ttc atc cct ttc ctc ctc att gtt gtt tcc tat gtc      289
Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
          85                      90                      95

cgg atc ctt caa tct gtt ctc agg atg cgg tca gcc tcc ggg cgg tat      337
Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
          100                      105                      110

aag gca tta tcc acc tgt acc tcc cat ttg aca gtg gta acc tta ttt      385
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
          115                      120                      125

tat ggg act gcc atc ctc atg tac atg aga cca cag tcg agg tct tcc      433
Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
          130                      135                      140

tgg gct ggc ggc aag atc att gcg gtt ttc tac acg gtg gtc aca ccc      481
Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
          145                      150                      155                      160

atg ctt      487
Met Leu

```

<210> 211

<211> 162

<212> PRT

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750

<400> 211

```

Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
1              5              10              15

```

Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
 20 25 30

Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
 35 40 45

Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
 50 55 60

Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
 65 70 75 80

Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
 85 90 95

Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
 100 105 110

Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
 115 120 125

Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
 130 135 140

Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 212

<211> 488

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9593; gene = GG0101; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF179751

<400> 212

tgtggccatt agccaccac ttcactatcc catcctcatg aatcagaggg tctgtctcca 60

gattaccggg agctcctggg cctttgggat aatcgatggc tttgatccag atggtggtag 120

```

taatgaattt ccctactgt ggcttgagga aggtgaacca tttcttctgt gagatgctat 180
ccttggtgaa gctggcctgt gtagacacat ccctgtttga gaaggtgata tttgcttgct 240
gtgtcttcat gcttctcttc ccattctcca tcatcgtygc ctcctatgct cgcattctag 300
ggactgtgct gcaaatgcac tctgctcagg cctggaaaaa ggccctggcc acctgctcct 360
cccacctgac agctgtcacc ctcttctatg gggcagccat gttcatctac ctgaggccta 420
ggcgctaccg ggcccccagc catgacaagg tggcctctat cttctacaca gtccttactc 480
ccatgctg 488

```

<210> 213

<211> 487

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9593; gene = GG0102; Accession DDBJ/EMBL/GenBank = AF179752

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 213

```

t gtt gtc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag 49
Val Val Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

```

```

ttc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc 97
Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

```

```

tcc ctc tct cac acc gtt ctc ctg acc cag ctg tct ttc tgt gct gcg 145
Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
35 40 45

```

```

aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

```

```

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

```

```

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggt 289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

```

```

tac att ggg gcc acc atc ctg ggg gtc cct tca acc aaa ggg atc cac 337
Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His

```

222

100						105						110						
aaa	gca	ttg	tcc	aca	tgt	ggc	tcc	cat	ctc	tct	gtg	gtg	tct	ctc	tat	385		
Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Tyr			
115						120						125						
tat	ggg	tca	ata	ttt	ggc	cag	tac	ctt	ttc	ccg	act	gta	agc	agt	ttt	433		
Tyr	Gly	Ser	Ile	Phe	Gly	Gln	Tyr	Leu	Phe	Pro	Thr	Val	Ser	Ser	Phe			
130						135						140						
att	gac	aag	gat	gtc	att	gtg	gct	ctc	atg	tac	acg	gtg	gtc	aca	ccc	481		
Ile	Asp	Lys	Asp	Val	Ile	Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro			
145						150		155						160				
acg	ttg															487		
Thr	Leu																	

```
<210> 214
<211> 162
<212> PRT
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9593; gene = GG0102; Accession DDBJ/EMBL/GenBank = AF179752
<400> 214
```

Val Val Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His

100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Thr Leu

<210> 215
<211> 488
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9593; gene = GGO103; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179753

<400> 215
tgcggtgtgc tgccacccac tccgatatcc cactctcatg agctggcagc tgtgcctgag 60
gataaccatg ttgtcttggc tcttgggtgc agctgacggg ctcatgcagg ctgttgctac 120
cctgagcttc ccatattgcg gtgcacacga gatcgatcac ttcttctgcg aggccccgt 180
gctggttcat ttggcttgtg ctgacacttc agtcttcgaa aacgccatgt acatctgctg 240
tgtgttaatg ctcttgggtcc ccttttccct catcctgtcc tcctatgggc tcatcctcgc 300
tgctgttctg cacatgcgct ctacagaagc ccgcaagaag gcctttgcca cctgctcttc 360
acatttggtg gtggtgggac tcttttatgg agctgccatt tttacctata tgagacccaa 420
atcccacagg tccactaacc acgataaggt tgtgtcagcc ttctatagta tgttcacccc 480
tttactaa 488

<210> 216
<211> 458
<212> DNA
<213> Gorilla gorilla
<220>
<221> misc_feature

<222> (1)..(458)

<223> Taxon = 9593; gene = GGO104; pseudogene; Accession DDBJ/EMBL/GenBank = AF179754

<400> 216

```
ccaccatcat gagtcacagc cagtgtgtca tgctggtggc tgggtcctgg gtcacgctt      60
gtgcgtgtgc tcttttgcac accctcctcc tggcccggct ttccttctgt gctgaccaca    120
tcacccctca cttcttctgt gaccttgggt ccctgctcaa gttgtcctgc tcagacacct    180
ccctcaatca gttagcaatc ttacagcag gattgacagc cattatgctt ccattcctgt    240
gcacccgtgt ttcttatggt cacattgggg tcaccatcct ccagattccc tctaccaagg    300
gcatatgcaa agccttgtcc acttgtggat cccacctctc agtggtgact atctattatg    360
ggacaattat tgggtctctat tttcttcccc catcctgcaa caccaatgac gagaacataa    420
ttgcttcagt gatatacaca gtagtcactc ccatattg                                458
```

<210> 217

<211> 477

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(477)

<223> Taxon = 9593; gene = GGO106; Accession DDBJ/EMBL/GenBank = AF179755

<220>

<221> CDS

<222> (2)..(475)

<223> Product = olfactory receptor

<400> 217

```
t gtg gcc atc cgt aag ccc ttg cat tat ttg gtt atc atg aga caa tgg      49
Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
  1              5              10              15

gtg tgt gtt gtg ctg ctg gta atg tcc tgg gtt gga gga ttt ctg cac      97
Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
      20              25              30

tca gta ttt caa ctt agc att att tat ggg ctc cca ttc tgt ggc ccc      145
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
      35              40              45

aat gtc att gat cac ttt ttc tgt gac atg tat ccc tta ttg aaa ctg      193
Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
      50              55              60

gtc tgc act gac acc cat gtt att ggc ctc tta gtg gtg acc aat gga      241
Val Cys Thr Asp Thr His Val Ile Gly Leu Val Val Val Thr Asn Gly
      65              70              75              80
```


gga ctg tct tgc act att gtg ttt ctg ctc tta ctc atc tct tat ggt 289
 Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Ile Ser Tyr Gly
 85 90 95

gtc atc ttg cac tct cta aag aaa ctt agt cag aaa ggg agg caa aaa 337
 Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
 100 105 110

gcc ctc tca acc tgc agt tcc cac atc act gtg gtt gtc ttc ttc ttt 385
 Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe Phe
 115 120 125

gtt cct tgt att ttt atg tat gct aga cct gct agg agc ttc ccc att 433
 Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
 130 135 140

gac aaa tca gtg agt gtg ttt tat aca gtc ata acc cca atg ct 477
 Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
 145 150 155

<210> 218

<211> 158

<212> PRT

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(477)

<223> Taxon = 9593; gene = GGO106; Accession DDBJ/EMBL/GenBank = AF179755

<400> 218

Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
 1 5 10 15

Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
 20 25 30

Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
 35 40 45

Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
 50 55 60

Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
 65 70 75 80

Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Ile Ser Tyr Gly
 85 90 95

Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
 100 105 110

Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe Phe
 115 120 125

Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
 130 135 140

Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
 145 150 155

<210> 219

<211> 488

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9593; gene = GGO107; Accession DDBJ/EMBL/GenBank = AF179756

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 219

t ctt gcc atc tgc tat cct tta cac tac gga gcc atg atg agt agc ctg 49
 Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly Ala Met Met Ser Ser Leu
 1 5 10 15

ctc tca gtg cag ttg gcc ctg ggc tcc tgg gtt tgt ggt ttc atg gcc 97
 Leu Ser Val Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Met Ala
 20 25 30

att gca gtg ccc aca gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc 145
 Ile Ala Val Pro Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro
 35 40 45

cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg 193
 Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
 50 55 60

gcc tgc acc aac aca cag gca gta gag ctt gtg gcc ttt gtg att gct 241
 Ala Cys Thr Asn Thr Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala
 65 70 75 80

gtt gtg gtt atc ctg agt tca tgc ctc atc acc ctt gtc tcc tat gtg 289
 Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
 85 90 95

```

tac atc atc agc acc atc ctc agg atc ccc tct gcc agt ggc cgg agc      337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
      100              105              110

aaa gcc ttc tcc acg tgc tcc tcg cat ctc acc gtg gtg ctc att tgg      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
      115              120              125

tat ggg tcc aca att ttc ctt cac gtc cgc acc tct atc aaa gac gcc      433
Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala
      130              135              140

ttg gat ctg atc aaa gct gtc cac gtc ctg aac act gtg gtg act cca      481
Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
145              150              155              160

gtt tta a                                                                488
Val Leu

```

```

<210> 220
<211> 162
<212> PRT
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9593; gene = GGO107; Accession DDBJ/EMBL/GenBank = AF179756
<400> 220

```

```

Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly Ala Met Met Ser Ser Leu
1              5              10              15

```

```

Leu Ser Val Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Met Ala
      20              25              30

```

```

Ile Ala Val Pro Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro
      35              40              45

```

```

Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
50              55              60

```

```

Ala Cys Thr Asn Thr Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala
65              70              75              80

```

```

Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
      85              90              95

```

Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
 115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala
 130 135 140

Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
 145 150 155 160

Val Leu

<210> 221
 <211> 480
 <212> DNA
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(480)
 <223> Taxon = 9593; gene = GGO108; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF179757
 <400> 221

tgtggcgggtg tgtaaccctc ttctctacac agttgcaatg tcccagaggc ttgctcctt 60
 gttggtggct acatcatact gttgggggac agtctgttcc ctgacaccta ctttctactg 120
 gaattatcct tcagaggaaa taatatcatt aataactttg tctgtgagca cgctgtcatt 180
 gttgctgtgt cttgctctga cccctatttg agccaggaga tcactttagt ttctgccaac 240
 attcaatgaa ataagcagcc tggatgatcat tctcacttcc tatgctttca tttttatcac 300
 tgtcatgaag acgccttcca ctggggggcg caagaaagcg ttctccacgt gtgcctccca 360
 cttgacggcc attaccattt tccatgggac tacccttttc ctctactgtg ttccctaactc 420
 aagttcgcggt ctcattgtca aggtggcctc tgtctttttg acagtgggtca ttcccatgtg 480

<210> 222
 <211> 487
 <212> DNA
 <213> Gorilla gorilla
 <220>
 <221> misc_feature

<222> (1)..(487)
<223> Taxon = 9593; gene = GGO109; Accession DDBJ/EMBL/GenBank = AF179758
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 222
t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cac agc 49
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctc ctg gcc cgg ctt tcc ttc tgt gct gac 145
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35 40 45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg 193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga 241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt 289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc 337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat 385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc 433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

atg ttg 487
Met Leu

<210> 223

<211> 162

<212> PRT
<213> Gorilla gorilla
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9593; gene = GGO109; Accession DDBJ/EMBL/GenBank = AF179758
<400> 223

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 224
<211> 487

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<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA1; Accession DDBJ/EMBL/GenBank = AF179759
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 224
t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa      49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
    1             5             10             15

ctc agc gct cag ttg cta agt att tca tat gta att ggt ttc ctg cat      97
  Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
    20             25             30

cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt      145
  Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
    35             40             45

aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att      193
  Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
    50             55             60

tca tgc aat ggt cca tct att aac gca cta ata ata ttt att ttt ggt      241
  Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Ile Phe Ile Phe Gly
    65             70             75             80

gct ttt ata caa ata ccc act tta atg act atc ata atc tct tat act      289
  Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
    85             90             95

cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc      337
  Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
    100            105            110

aaa gcc ttc tcc aca tgc ggc gcc cat ctg ctt tct gtc tca ttg tac      385
  Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
    115            120            125

tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct      433
  Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
    130            135            140

gaa gac caa gac aaa gtg tat tct ctg ttt tac acg att ata att ccc      481
  Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
    145            150            155            160

ctg cta      487
Leu Leu

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<210> 225
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA1; Accession DDBJ/EMBL/GenBank = AF179759
<400> 225

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15

Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30

Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45

Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
50 55 60

Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Ile Phe Ile Phe Gly
65 70 75 80

Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
85 90 95

Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
115 120 125

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
130 135 140

Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145 150 155 160

Leu Leu


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<210> 226
<211> 487
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA10; Accession DDBJ/EMBL/GenBank = AF179760
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 226
t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag      49
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
  1             5             10             15

ctc tgt gtc ttc tta gtg gct gta tct cgg att ctg tct tgt gcc agc      97
Leu Cys Val Phe Leu Val Ala Val Ser Arg Ile Leu Ser Cys Ala Ser
      20             25             30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg      145
Ser Leu Ser His Thr Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35             40             45

aac acc gtc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50             55             60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85             90             95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100            105            110

aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115            120            125

tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130            135            140

att gac aag gat gtc att gtg gct ctc atg tac acg gtg gac aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Asp Thr Pro
      145            150            155            160

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atg ttg
Met Leu

487

<210> 227
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA10; Accession DDBJ/EMBL/GenBank = AF179760
<400> 227

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Val Ser Arg Ile Leu Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Asp Thr Pro
145 150 155 160

Met Leu

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<210> 228
<211> 487
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA12; Accession DDBJ/EMBL/GenBank = AF179761
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 228
t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
    1             5             10             15

ctc tgt ctc gcc ctg gtg ggc ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
      20             25             30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
      35             40             45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
      50             55             60

gcc ttc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga      241
Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
      65             70             75             80

ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
      85             90             95

aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
      100            105            110

aag gcc ctc tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
      115            120            125

tat gga acc gtt att ggt ctc tac tta tgc tca tca gct aat agt tct      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
      130            135            140

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act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 229
 <211> 162
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9606; gene = HSA12; Accession DDBJ/EMBL/GenBank = AF179761
 <400> 229

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 230
 <211> 486
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9606; gene = HSA13; pseudogene; Accession DDBJ/EMBL/GenBank = AF179762
 <400> 230
 cgtggctgtg tgtaaccccc tcctctatgc catagtcatg acaccaatga cccgcctggc 60
 gctgctggcc ggggcatatt ctggtgcat agtcaattct gtgatctgca ctggctgcac 120
 cttctctatc tccttctcta agtccaacca ttagacttc ttttctgtg acctcccacc 180
 cctgctgaag ctgacctgta gtgaaaccag gccacgggaa tgggtgatct acctctcagc 240
 ttttctggtc atcacaacca gcatttcagt gattcttaca tcgtacttgt tcatcattca 300
 gtctattctg aagattcgta cagcaggtgg aaagccaaga ccttctccac ctgtgcttct 360
 cacaagactg cattgactct cttctttgga aactcatat tcatatacct gaaaggcaac 420
 atgggcgaat cccttgagga agacaagatc gtgtcaatat ttactactgt ggtcatcccc 480
 atgcta 486

<210> 231
 <211> 487
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9606; gene = HSA16; pseudogene; Accession DDBJ/EMBL/GenBank = AF179763
 <400> 231
 catggccatt gtgaaccctt tactttatac agtagctatg actaaaatag tttgtattgt 60
 gctcgcatth gggatcatgta tgggaggttt aatcagctca ttgacacata caattggctt 120
 ggtgaaactg tctttctgtg ggccaaatgt catcagtcac ttcttctgtg atcttcccc 180

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actgttgaag ctgtcatggt ctgagacatc tatgaatgaa ttgttgcttt tgatcttctc 240
tggcattatt gccacgctca cttttttgac tgtgggtgatc tectacatct tcattgttgc 300
tgctatcctg aggatccgct aagaagcagg tagacgtaaa gccttctcca cctgcacctc 360
tcacctgatt accgtgacct tattctatgg atcgataagc tttagttaca ttcagccaaa 420
ctcccagtat tccctagaac aagaaaagggt ggtgtctgta ttttataccc tgggtggttcc 480
tatgtta 487

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<210> 232
<211> 485
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 9606; gene = HSA18; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179764
<400> 232

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cgtgggcac tgtaaccac tgttgtacac ggtcaccatg tctccccaga agtggttgct 60
ccttttactg ggtgtctatg ggatggggat tttggggctg tggctcatat gggaaacata 120
atgtttatgt ccttttgtgg agacaacctt gtcaatcact atatgtgtga catccttctc 180
ctccttgagc tctcctgcaa cagctcttac ataaatttgc tgggtggtttt tattattgtg 240
accgttggca ttgggggtgcc gattgtcacc atttttctct cttatggttt tattctttcc 300
agcattctcc acattagttc cacagagggc aggtctaaag ccttcagtac ctgcagttcc 360
cacataattg tggatatcgt ttctttgggt caggtgcttt catgtacctc aaaccacctt 420
ctattctacc cctggaccag gggaaagtgt cctccatttt ttgtactgct gtggtgcccc 480
tgttt 485

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<210> 233
<211> 486
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9606; gene = HSA2; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179765
<400> 233
cgtgggcac tgtaaccac tgttgtacac ggtcaccatg tctccccaga tgtgttgct 60

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ccttttactg ggtgtctatg ggggtgggat tttggggctg tggctcatat gggaaacata 120
atgtttatgt ccttttgtgg agacaacctt gtcaatcact atatgtgtga catccttcct 180
ctccttgagc ctcctgcaa cagctcttac ataaatttgc tgggtggtttt tattattgtg 240
accgttgga tgggggtgcc gattgtcacc atttttctct cttatggttt tattctttcc 300
agcattctcc acattagttc cacagagggc aggtctaaag ccttcagtac ctgcagttcc 360
cacataattg tggtatcgct tttctttggg tcaggtgctt tcatgtacct caaacacct 420
tctattctac ccttggacca ggggaaagtg tcctccattt tttgtactgc tgtggtgccc 480
atgttt 486

```

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<210> 234
<211> 487
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA3; Accession DDBJ/EMBL/GenBank = AF179766
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 234
t gtg gcc atc tgt aaa ccc ctt cat tat gtg gtc atc atg aac aac agg 49
Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
1 5 10 15

gtg tgt acc tta tta gtt ctc tgc tgt tgg gtg gct ggc ttg atg atc 97
Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
20 25 30

att gtt cca cca ctt agc tta ggc ctc cag ctc gaa ttc tgt gac tcc 145
Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
35 40 45

aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc 193
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
50 55 60

tca tgc tca gat aca tgg gta ata gaa cag atg gtt ata ctt atg gct 241
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65 70 75 80

gta ttt gca ctc att atc acc cca gtt tgt gtg att ctg tcc tac ttg 289
Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
85 90 95

```

```

tac ata gtc aga aca att ctg aag ttc cct tct gtt cag caa agg aaa      337
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
      100                      105                      110

aag gcc ttt tct acc tgt tca tcc cac atg att gtg gtt tcc att gcc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
      115                      120                      125

tat gga agc tgc atc ttc atc tat atc aag ccc tct gca aaa gat gag      433
Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
      130                      135                      140

gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtc gca ccc      481
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
      145                      150                      155                      160

ttg ttg                                                                487
Leu Leu

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<210> 235
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA3; Accession DDBJ/EMBL/GenBank = AF179766
<400> 235

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Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
1                      5                      10                      15

```

```

Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
      20                      25                      30

```

```

Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
      35                      40                      45

```

```

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
      50                      55                      60

```

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Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65                      70                      75                      80

```

```

Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
      85                      90                      95

```


Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
 115 120 125

Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 130 135 140

Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
 145 150 155 160

Leu Leu

<210> 236

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9606; gene = HSA5; Accession DDBJ/EMBL/GenBank = AF179767

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 236

t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15

ctc tgt gtc ttc tta gtg gct gta act tgg att ctg tct tgt gcc agc 97
 Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
 20 25 30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg 145
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45

aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

```

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85                      90                      95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100                    105                    110

aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115                    120                    125

tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130                    135                    140

att gac aag gat gtc att gtg gct ctc atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
      145                    150                    155                    160

atg ttg      487
Met Leu

```

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<210> 237
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA5; Accession DDBJ/EMBL/GenBank = AF179767
<400> 237

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```

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1              5              10              15

```

```

Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
      20              25              30

```

```

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35              40              45

```

```

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50              55              60

```

```

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65              70              75              80

```

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 238

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(478)

<223> Taxon = 9606; gene = HSA6; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179768

<400> 238

tgttgccatc tgtaaccctt tgcgctacct tacagtcattg aacccccagc tatgcctttg 60

gttggttctt gcctgctggt gtgggggttt tatccactct atcatgcagg tcatactagt 120

catccagctg cctttctgtg ggcccaatga actggacaac ttctactgtg atgtcctaca 180

aatcatcaag ctggcctgca tggacaccta tgtggttagag gtgctggtga tagccaacag 240

tggctctgtg tctcttgtct gcttcttggt cttactattc tcttatgcta tcatcctgat 300

caccctgaga acacgcttct gccagggcca gaacaaggta ctctctacct gtgcttctca 360

cctgacagtg gtcagcctga tcttcgtgcc atgcgtattc atctatttga ggcctttctg 420

cagcttctct gtggataaga tattctcctt gttttacaca gtgattacac ctatgttg 478

<210> 239

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<211> 488
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9606; gene = HSA7; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179769
<400> 239
catggccatc tgcaagccct tggtatatgg aagcaaatg accaggtgtg tctgcctctg   60
tctggctgct gctccctata tttatggctt tgcaaatggc ctaagcacag accaccctga   120
tgcttcgtct gtccttctgt ggacccaatg acatcaacca cttttactgt gcggacccac   180
ccctcttagt cctcgcttgc tcagatactt atgtcaaaga gaccgccatg ttggtgggtg   240
ctgggttcaa cctcatttgc tctctcaccg tcctcctcat ttctacact ttcatttca   300
ctgccattct gcgtatccac actgctgagg ggaggcgcaa ggccttctcc acctgcgggt   360
ctcatgtgac cgctgtcact gtcttctatg ggacactggt ctgcatgtac ctgaggcccc   420
cttctgagac atctatacaa caggggaaaa ttgtagctgt tttttatatc tttgtgagtc   480
cgatgtta                                         488

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<210> 240
<211> 487
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA8; Accession DDBJ/EMBL/GenBank = AF179770
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 240
t gtt gcc atc tgc aag ccc ctt cat tac aca tcc atc atg aac agg aaa   49
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
1          5          10          15

ctc tgc act cta ctt gtg ctg tgt gcc tgg cta agt ggg ttt ctg acc   97
Leu Cys Thr Leu Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr
20          25          30

att ttc cca ccc ctt atg ctt ctc ctc cag ctg gat tac tgt gct tcc   145
Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser
35          40          45

aac gtc att gat cac ttt gca tgt gac tat ttt ccc ctc tta caa cta   193

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Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50                      55                      60

tct tgt tca gat aca tgg ctc cta gaa gta att ggt ttt tac ttt gct      241
Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
65                      70                      75                      80

ttg gtt act ttg ctg ttc act ttg gca tta gtg att tta tct tac atg      289
Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
                      85                      90                      95

tac att atc agg acc att ttg aga atc ccg tct gcc agt caa aga aaa      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
                      100                      105                      110

aag gct ttc tcc act tgt tct tct cac atg att gtc att tcc att tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
                      115                      120                      125

tat gga agc tgt ata ttc atg tat gct aat cca tct gca aaa gaa aag      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
130                      135                      140

gca tca ttg aca aaa gga ata gct att ctc aat aca tct gtt gcc ccc      481
Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
145                      150                      155                      160

atg ctg      487
Met Leu

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<210> 241
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA8; Accession DDBJ/EMBL/GenBank = AF179770
<400> 241

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Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
 1                      5                      10                      15

Leu Cys Thr Leu Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr
20                      25                      30

Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser
35                      40                      45

```

Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
65 70 75 80

Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
130 135 140

Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Met Leu

<210> 242

<211> 485

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 13515; gene = EFU145; Accession DDBJ/EMBL/GenBank = AF179771

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 242

t gtg gcc atc tgc cag cca ctc caa tac agc aca gct atg agt cac cag 49
Val Ala Ile Cys Gln Pro Leu Gln Tyr Ser Thr Ala Met Ser His Gln
1 5 10 15

ctc tgt gca ctc atg ctg gcc atg tgc tgg ctg cta acc aac tgt cct 97
Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
20 25 30

gca ttg atg cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag 145

Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
 35 40 45

agg gcc atc ccc cac ttc tac tgt gat ccc agt gct ctc ctg aag ctc 193
 Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
 50 55 60

gcc tgc tcg gat acc cgc ata aac gag ctg atg atc atc gcc atg ggc 241
 Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
 65 70 75 80

ttg gcc ttc ctc acg gtt ccc ctc acg ctg atc gtc ttc tcc tac gtc 289
 Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
 85 90 95

cgc atc tcc tgg gct gtg ctt ggc atc tcg tct cct gga ggg cga tgc 337
 Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
 100 105 110

aaa gcc ttc tcc acc tgt ggt tct cat ctc acg gtg gtt ctg ctc ttc 385
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
 115 120 125

tat ggg tct ctt atg ggt gtg tat ttg ctt cct ccg tca tct tac tct 433
 Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
 130 135 140

aca gag agg gaa agc agg gct gcc att ctc tac atg gtg atc att ccc 481
 Thr Glu Arg Glu Ser Arg Ala Ala Ile Leu Tyr Met Val Ile Ile Pro
 145 150 155 160

atg t 485
 Met

<210> 243

<211> 161

<212> PRT

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 13515; gene = EFU145; Accession DDBJ/EMBL/GenBank = AF179771

<400> 243

Val Ala Ile Cys Gln Pro Leu Gln Tyr Ser Thr Ala Met Ser His Gln
 1 5 10 15

Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
 20 25 30

Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
35 40 45

Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
65 70 75 80

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
85 90 95

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
115 120 125

Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
130 135 140

Thr Glu Arg Glu Ser Arg Ala Ala Ile Leu Tyr Met Val Ile Ile Pro
145 150 155 160

Met

<210> 244

<211> 485

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 13515; gene = EFU146; pseudogene; Accession DDBJ/EMBL/Genbank = AF179772

<400> 244

cgttgccatc tgcaagcccc tccactaccc ggtgctcatg agcagcaggg tctgcacaca 60

gctcatcctc gcctgctggc tggcagggtt ctccttcacg attgtgcctg tcatcctgac 120

cagtcagctt ccattctgtg acaccacat caaccacttc ttctgtgact atacacctct 180

aatggaggtg gtctgcagtg ggccaaaggt gctggagatg gtggatttta ccctggcctt 240

ggtggcaccg ctcagcacct tgggtgctgat caccctgtcc tacatccaga tcatcagcac 300
 gattgtcagg atcccctctg tccaggagag gaaaaaggct ttctccacct gttcctccca 360
 tgtcatcgtg gttacatgt gctatggaaa gctgtttttt tatgtatgtc aagccctccc 420
 caggcaaagg ggttgatcta aacaaaggag tgtctctaata caatacagtt attgcccccc 480
 tcttg 485

<210> 245

<211> 487

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 13515; gene = EFU147; Accession DDBJ/EMBL/GenBank = AF179773

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 245

c gtg gcc atc tgc ctt cct ctg cac tac acc atg gtc atg aaa ccc cga 49
 Val Ala Ile Cys Leu Pro Leu His Tyr Thr Met Val Met Lys Pro Arg
 1 5 10 15

tgc tgc ctg atg ctg gtg gca gca tcc tgg ctc tgc tcc cac tgc ctg 97
 Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
 20 25 30

gct ttc tct ctc acc ctt ctg atg act cag ttc tca ttc tgt gcc tcc 145
 Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
 35 40 45

cat tcc atc caa cac ttt ttc tgt gat gta ccc cca ctc ctc aaa ctt 193
 His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
 50 55 60

gcc tgt tca gac acc cat atc ttt cag gtc aca atg tta act gaa gga 241
 Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
 65 70 75 80

gtc ctc tca ggt gtg atc cct ctt acc tgt gtc ctg gtc tct tat gcc 289
 Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
 85 90 95

cac atc atg cac acc atc ctc agg atc cct tct gct ggg ggc aag cac 337
 His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
 100 105 110

aaa gtc ttc tct acc tgt ggc tct cac ctg tca gtg gtc act ctc ttc 385
 Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe

```

      115              120              125
tat ggg acc ctc ttt ctg gtg tat ttc cag cct tca tcc tcc tac tca      433
Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
      130              135              140

gca gat act gga atg gtg gca tgt gta gta tac acg atg gtc acc ccc      481
Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
145              150              155              160

atg gtg      487
Met Val

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<210> 246
<211> 162
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU147; Accession DDBJ/EMBL/GenBank = AF179773
<400> 246

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Val Ala Ile Cys Leu Pro Leu His Tyr Thr Met Val Met Lys Pro Arg
1              5              10              15

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Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
      20              25              30

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Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
      35              40              45

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His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
      50              55              60

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Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
      65              70              75              80

```

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Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
      85              90              95

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His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
      100              105              110

```

```

Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe

```

115

120

125

Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
 130 135 140

Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
 145 150 155 160

Met Val

<210> 247

<211> 487

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 247

t gtg gcc atc tgc aaa ccg ctg cat tat gtg gcc att atg agt aac aca 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
 1 5 10 15

gtc tgc aga aga ctt gtc ttt tgt tgt tgg gta gct ggt ctg ttt att 97
 Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
 20 25 30

ata atc cct cca ctt agc ctg ggc cta aat ctg gaa ttt tgt gat tct 145
 Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser
 35 40 45

gat acc att gat cat ttt atc tgt gat gca tct ccc ctc ctg aat atc 193
 Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile
 50 55 60

tct tgt tca aat act tgg ttc atg gaa cag act gtt atc atc tgt gca 241
 Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala
 65 70 75 80

gtg ctg acc ctc att atg aca ctt atg tgt gta gtt ctg tcc tac att 289
 Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile
 85 90 95

tat atc atc aag aca att tta gga ttc tct tct gcc cag caa aag aaa 337
 Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys

100 105 110
aaa gcc ttt tcc acc tgt tct tcc cac atg att gtg gtg tcc atc acc 385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr
115 120 125
tat ggc agc tac atc ttc atc tat atc aaa cct tct gca aag gaa gaa 433
Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu
130 135 140
gta gcc att aac aag ggt gtg aca gtc ctc act act tcc atc gcc ccc 481
Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro
145 150 155 160
atg ctg 487
Met Leu

<210> 248
<211> 162
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774
<400> 248

Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
1 5 10 15

Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
20 25 30

Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser
35 40 45

Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile
50 55 60

Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala
65 70 75 80

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile
85 90 95

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys

100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr
 115 120 125

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu
 130 135 140

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro
 145 150 155 160

Met Leu

<210> 249
 <211> 487
 <212> DNA
 <213> Eulemur fulvus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 249

t gtt gct atc tgt aag ccc ctg cat tac agg gtc atc atg aat cga aga 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
 1 5 10 15

gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc 97
 Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
 20 25 30

gta ttc cca gca ctc atg ttg ctc tta aag ctt gat tac tgt gga ttt 145
 Val Phe Pro Ala Leu Met Leu Leu Lys Leu Asp Tyr Cys Gly Phe
 35 40 45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt 193
 Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60

tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct 241
 Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
 65 70 75 80

gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg 289
 Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met

	85	90	95	
cac atc gtg aga acg att ttg aga att cct tct act agt cag agg aca				337
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr				
	100	105	110	
aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct				385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser				
	115	120	125	
tat ggc agc tgc att ttt atg tac att aag ccc tca gca aag gat aga				433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg				
	130	135	140	
gta tct ttg agc aag gca gtg gct gtg cta atc acc tca gta gct ccc				481
Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro				
	145	150	155	160
atg ctc				487
Met Leu				

<210> 250
 <211> 162
 <212> PRT
 <213> Eulemur fulvus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775
 <400> 250

Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg				
1	5	10	15	

Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile				
20	25	30		

Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe				
35	40	45		

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu				
50	55	60		

Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala				
65	70	75	80	

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met				
---	--	--	--	--

85

90

95

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
145 150 155 160

Met Leu

<210> 251

<211> 484

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 13515; gene = EFU150; pseudogene; Accession DDBJ/EMBL/GenBank = AF179776

<400> 251

tctggctatc tgctatcctc tacactacgg gacaatcatg agcagcctgc tggctgcaca 60

gctggccttg ggctcctggg tctgtggttt cctggccatt gcagtgcctga cggcccttat 120

cagtggcctg tccttctgtg gcgcccgtgc catcaatcac ttcttctgtg acattgcacc 180

ctggatcgcc ctggcctgta ccagcacaca ggcaatagag ctctggcct ttgtgattgc 240

ttttgtggtc atcctgagtt catgcctcat caccctgggc tcctacgtgt acattatcag 300

caccatcctc aggatcccat ctgccagcgg cggagcaaag ccttctctac gtgctcctct 360

cacctaccg tgggtgctcat ctggtatggg tccacgattt ttcttcatgt ccgcacctcc 420

atcacagacg ccttggatct gaccaaagct gtccatgtcc tgaacaccgt ggtgactcca 480

gttc 484

<210> 252

<211> 487

<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 252
t ctg gct atc tgc tat cct cta cac tac agg aca atc atg agc agc ctg 49
Leu Ala Ile Cys Tyr Pro Leu His Tyr Arg Thr Ile Met Ser Ser Leu
1 5 10 15
ctg gct aca cag ctg gcc ttg ggc tcc tgg gtc tgt ggt ttc ctg gcc 97
Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
20 25 30
att gca gtg ctg acg gcc ctt atc agt ggc ctg tcc ttc tgt ggc gcc 145
Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
35 40 45
cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg 193
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
50 55 60
gcc tgc acc agc aca cag gca ata gag ctc gtg gcc ttt gtg att gct 241
Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
65 70 75 80
ttt gtg gtc atc ctg agt tca tgc ctc atc acc ctg gtc tcc tac gtg 289
Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
85 90 95
tac att atc agc acc atc ctc agg atc cca tct gcc agc ggc cgg agc 337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
100 105 110
aaa gcc ttc tct acg tgc tcc tct cac ctc acc gtg gtg ctc atc tgg 385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
115 120 125
tat ggg tcc acg att ttt ctt cat gtc cgc acc tcc atc aca gac gcc 433
Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
130 135 140
ttg gat ctg acc aaa gct gtc cat gtc ctg aac acc gtg gtg act cca 481
Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
145 150 155 160
gtt cta 487
Val Leu

<210> 253
<211> 162
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777
<400> 253

Leu Ala Ile Cys Tyr Pro Leu His Tyr Arg Thr Ile Met Ser Ser Leu
1 5 10 15

Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
20 25 30

Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
35 40 45

Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
50 55 60

Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
65 70 75 80

Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
85 90 95

Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
130 135 140

Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
145 150 155 160

Val Leu

```

<210> 254
<211> 487
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU153; Accession DDBJ/EMBL/GenBank = AF179778
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 254
t gtt gct atc tgt aag ccc ctg cat tac agg gtc atc atg aat cga aga      49
  Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
    1             5             10             15

gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc      97
  Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
        20             25             30

gta ttc cca gca ctc atg ttg ctc tta aag ctt gat tac tgt gga ttt      145
  Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe
        35             40             45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt      193
  Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
        50             55             60

tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct      241
  Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
        65             70             75             80

gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg      289
  Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met
        85             90             95

cac atc gtg agg acg att ttg aga att cct tct act agt cag agg aca      337
  His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
        100            105            110

aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct      385
  Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
        115            120            125

tat ggc agc tgc att ttt atg tac att aag ccc tca gca aaa gat aga      433
  Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
        130            135            140

gta tct ttg agc aag gca gtg gct gtg cta atc acc tca gta gct ccc      481
  Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
        145            150            155            160

```

atg ctc
Met Leu

487

<210> 255
<211> 162
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU153; Accession DDBJ/EMBL/GenBank = AF179778
<400> 255

Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
1 5 10 15

Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
20 25 30

Val Phe Pro Ala Leu Met Leu Leu Lys Leu Asp Tyr Cys Gly Phe
35 40 45

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
65 70 75 80

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met
85 90 95

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
145 150 155 160

Met Leu

```

<210> 256
<211> 488
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 256
c atg gcc atc tgc cat ccg ctc cgt tac cct gtc ttc atg aac cac agg      49
  Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg
    1             5             10             15

gtg tgt ctc ttc ctg gca tct ggc tgc tgg ttc ctg gga tca gta gat      97
Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp
    20             25             30

ggc ttc atg ctc act cca atc acc atg acc ttc ccc tac tgc agg tcc      145
Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser
    35             40             45

cgg gag att cac cat tcc ttc tgc gaa gtc cct gct gta acg acg ctt      193
Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu
    50             55             60

tcc tgc tca gac acc tca ctc tat gaa atg ctc atg tac ctg tgc tgt      241
Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys
    65             70             75             80

gtc ctc atg ctc ctc att cct gtg aca gtc att tca agc tcc tat tca      289
Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser
    85             90             95

ttc att ctc ctc acc atc cac agg atg ggc tca gca gag ggc cgg aag      337
Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys
    100            105            110

aag gcc ttt gcc acc tgt tcc tcc cac atg acc gtg gtt atc ctc ttc      385
Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe
    115            120            125

tat ggg gcc gcc atc tac acc tac atg ctc ccc agc tcc tac cac act      433
Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
    130            135            140

```

cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct 481
Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro
145 150 155 160

gtg cta a 488
Val Leu

<210> 257
<211> 162
<212> PRT
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779
<400> 257

Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg
1 5 10 15

Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp
20 25 30

Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser
35 40 45

Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys
65 70 75 80

Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser
85 90 95

Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys
100 105 110

Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe
115 120 125

Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
130 135 140

Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro
145 150 155 160

Val Leu

<210> 258
<211> 488
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 13515; gene = EFU155; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179780
<400> 258
tgttgctatc tgtaagcccc tgcattacaa ggcatcatg aatcgaagag tcgtgcacac 60
tgctcgtctt tgccctcttgg ctggtttcat tcttaatcgt attcccagca ctcatgttgc 120
tcttaaagct tgattactgt ggatttaata ttattgacca ttttacctgt gattattttc 180
ccctgctgca gctttcctgt tcagatacaa aattcctgga gataatgggg ttttcctgtg 240
ctgtgtttac tctaattgtc actttggcat taatatttct gtccatcatg cacatcgtga 300
gaacgatttt gagaattcct tctactagtc agaggacaaa ggccttttct acatgttctt 360
cccacatgat tgtcatctcc atctcttatg gcagctgcat ttttatgtac attaagccct 420
cagcaaagga tagagtatct ttgagcaagg cagtggctgt gctaatacacc tcagtagctc 480
ccatgcac 488

<210> 259
<211> 486
<212> DNA
<213> Eulemur fulvus
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 13515; gene = EFU156; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179781
<400> 259
tgtggccatc tgcaagcccc tgcattatgt gaccgtcatg aacagcagag tttgcaggat 60
tctcatcatc tggtgttggg tggctgggtt atgcataata atccctccac ttagcctggg 120
tttaaactca aaattctgtg actctaacat gattgatcat tttggttgcg atgcatttcc 180

```

cctggtgaaa atctcatgct cagacacatg gttcatggaa cagacgggta tcatctgtgc 240
tgtgtgacc ctgaatatga ctctaacttg tgtagttctg tcatacgctt acatcatcaa 300
gacaatTTTT agattccctt ctgtccagca aaggaaaaag gccttttcca cctgttcttc 360
ccacatgatt gtgggtttcca tcacctatgg cacgtgcatt ttcacttaca tgaatcctac 420
agcaaaggaa gaagtgaccg ttaataaagt agtttctttg ctcatttctt ctattttgct 480
acattg 486

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<210> 260

<211> 486

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 34829; gene = ERU157; pseudogene; Accession DDBJ/EMBL/GenBank = AF179782

<400> 260

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cgtggccatc tgccagccac cccaatacag cacagctatg agtccccagc tctgtgcact 60
catgctggcc atgtgctggc tgctaaccag ctgtcctgcg ttgatgcaca cgctgttgct 120
gaccctgtgt gctttctgtg cccagaaggc catccccac ttctactgtg atcccagtgc 180
tctcctgaag ctgcctgct cggatacccg cataaatgag ctgatgatca tcgccatggg 240
cttgacgttc ctcaactatt ccctcacact gatcgtcttc tcctacgtcc gcatctcctg 300
ggctgtgctt ggcatctcgt ctcttgccgg gcgatgcaag gccttctcca cctgtgggtc 360
tcatctcacg gtgggttctg tcttctatgg gtctcttatg ggtgtgtatt tgcttcctcc 420
gtcatcttac tctacagaga gggaaagcag gctgccattc tctacatggt gatcattccc 480
atgtta 486

```

<210> 261

<211> 484

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 34829; gene = ERU159; pseudogene; Accession DDBJ/EMBL/GenBank = AF179783

<400> 261

```

tgtggccatc tgcaaccac tgaggatatcc catcatcatg aacagggtgt tataagtgca 60

```

```

aatggctgca tgggtcttggga tcataggcta tctgatctcc ttagtgcaaa cagtcttgac 120
aatgatattg cctttctgtg gcaataatgt cattgatcat attacctgtg agatcctggc 180
tcttaaactc atatgctcag atatttccat gaatgtgctt atcatggcag tggcaagtat 240
tggtatattg gtgattcctc tgctgttcat ttttatctcc tatgtattca tcctctcttc 300
catcctgaga attaattctt ctgaggggag aaagaaagcc tttgcaacct gttcagccca 360
cctgactgtg gtcactcttat tctatgggtc agctcttttt atgtacatga agcctaagtc 420
aaagtacaca aaagtatctg atgaaatcat tgcactgtct tacggagtag taaccccaat 480
gttg 484

```

<210> 262

<211> 487

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU160; Accession DDBJ/EMBL/GenBank = AF179784

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 262

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t gtt gcc ata tgt cac cct ctc cac tac acc acc atc atg agg gaa gag 49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Met Arg Glu Glu
    1             5             10             15

```

```

ctc tgc acc tta ttg gtg gct ata tcc tgg ctc ctg tct tgt gcc agc 97
Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
    20             25             30

```

```

tcc ctc tcc cac acc ctt ctc ctg acc cgg ctg tcc ttc tgt gct gct 145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
    35             40             45

```

```

aat gtc att ccc aac ttc ttc tgt gac ctt gct gct ctg ctc aag ctg 193
Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
    50             55             60

```

```

tcc tgc tca gac atc ttc ctc aat gag ctg gtc atg ttt aca gta ggg 241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
    65             70             75             80

```

```

gtg gtg gtc att acc ttg cca ttc tta tgt atc ctg gta tct tac ggc 289
Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
    85             90             95

```



```

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc tgc      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
      100              105              110

aaa gca tta tcc acg tgt ggg tcc cat ctc tct gtg gtg tct ctg tac      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115              120              125

tac ggg gca ata ttt ggg cag tac ctt ttc cca gca tta agc aat tcc      433
Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
      130              135              140

att gac aag gac atc att gtg gct atg atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
      145              150              155              160

atg ttg      487
Met Leu

```

```

<210> 263
<211> 162
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU160; Accession DDBJ/EMBL/GenBank = AF179784
<400> 263

```

```

Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Met Arg Glu Glu
1              5              10              15

```

```

Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
      20              25              30

```

```

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35              40              45

```

```

Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50              55              60

```

```

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65              70              75              80

```

```

Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
      85              90              95

```

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
 130 135 140

Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 264

<211> 475

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(475)

<223> Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785

<220>

<221> CDS

<222> (2)..(475)

<223> Product = olfactory receptor

<400> 264

c gtg gca atc tgc aag cct ctt cat tac atg aat att atg agt cgt caa 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
 1 5 10 15

ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac 97
 Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
 20 25 30

tct att att cag att ttt atc acc atc caa tcg ccc ttt tgt ggt ccc 145
 Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
 35 40 45

aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt 193
 Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
 50 55 60

gcc tgc acc gac acc ttt gta gag ggg ctg act gtg ttg gcc aat agt 241
 Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
 65 70 75 80

ggc tta att ccc gtg tgc tcc ctg ttt atc ctg gtg tcc tcc tat atc 289
 Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
 85 90 95

att att ctg gtg cac ttg agg aaa cat tct gca gag ggg agg cac aaa 337
 Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
 100 105 110

gcc ctc tct acc tgt gcc tct cac atc acg gtg gtc att ttg ttt ttt 385
 Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
 115 120 125

gga cct gcc atc ttc ctc tac atg cga cct tcc tct acc ttc aca gaa 433
 Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
 130 135 140

gac aaa ctc atg ggt gtg ttg tac aca gtc atc acc ccc agt 475
 Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
 145 150 155

<210> 265

<211> 158

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(475)

<223> Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785

<400> 265

Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
 1 5 10 15

Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
 20 25 30

Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
 35 40 45

Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
 50 55 60

Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
 65 70 75 80

Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
 85 90 95

Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
 100 105 110

Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
 115 120 125

Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
 130 135 140

Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
 145 150 155

<210> 266

<211> 487

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 266

t gtg gcc atc tcc aac ccc ccg ctc tat gtt cag gcc atg cca agg aaa 49
 Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
 1 5 10 15

ctg tgc atc tgt ttc att atc tgt tca tac act gga ggc ttt gtt aat 97
 Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn
 20 25 30

gca ata ata tta acc agc aac aca ttc acg ttg gat ttt tgt ggt gac 145
 Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
 35 40 45

aat gtc atc gac gac ttt ttc tgt gat gtc cca ccc ctg gtg aag ttg 193
 Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
 50 55 60

gcc tgt gat gtg gaa ggg agc tac cag gct gtg ctg tac ttc ctc ctg 241
 Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu
 65 70 75 80

gcc tcc aac gtc atc tcc ccg gcc atg ctc atc ctc gcc tcc tac gtc 289
 Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val
 85 90 95

```

ttc atc atc gca gca gtc ttg agg gtc cgc tcc agc cgg ggc cgc ctc      337
Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu
      100                      105                      110

aag gcc ttc tcc acg tgc tcc tcc cac ctg atc tct gtt acc tta tac      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr
      115                      120                      125

tac ggc tcc att ctc tac atc tac tct cgc cca agt tcc agc tat tcc      433
Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser
      130                      135                      140

ctc gag agg gac aaa atg gtc tct acc ttt tac acc gtg ctg ttc ccc      481
Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro
      145                      150                      155                      160

acg ctc                                                                487
Thr Leu

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<210> 267

<211> 162

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<400> 267

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Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
1              5              10              15

```

```

Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn
      20              25              30

```

```

Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
      35              40              45

```

```

Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
      50              55              60

```

```

Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu
      65              70              75              80

```

```

Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val
      85              90              95

```

Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr
 115 120 125

Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser
 130 135 140

Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro
 145 150 155 160

Thr Leu

<210> 268
 <211> 478
 <212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(478)
 <223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787
 <220>
 <221> CDS
 <222> (2)..(478)
 <223> Product = olfactory receptor
 <400> 268
 t gtt gcc gta tgt aac cct ttg cat tac ctg acg gtc atg aac cgc cag 49
 Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln
 1 5 10 15
 ctc tgc ctt cag ttg gtt ttt gcc tgc tgg tgt ggg ggt ttc atc cac 97
 Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His
 20 25 30
 tct gtc aca cag gtt ata ctg gtc atc cag ctg ccc ttc tgt ggc ccc 145
 Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
 35 40 45
 aac aaa ttg gac agt ttc tac tgt gat gtc cca gag gtc atc aag ctg 193
 Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu
 50 55 60
 gcc tgc ctg gac acc tat gtg gta gaa gtg ctg atg gtt acc aac agt 241
 Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser
 65 70 75 80

ggc ctg cta tct ctt gtc tgc ttc ttg gtc ttg ata ttc tct tat gcc 289
Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala
85 90 95

acc atc ctg acc acc ctg aga act cgc ctc cac cag ggc cag agc aag 337
Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys
100 105 110

gcc ttc tct acc tgt gcc tcc cac cta atg gtg gtc agc ctg atc ttt 385
Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe
115 120 125

gtg cca tgt gta ttc atc tac ttg agg cct ttc tgc agc ttc tct gtg 433
Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
130 135 140

gat aag ata ttc tct gtg ttt tac atg gtg atc aca cct atg ttg 478
Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu
145 150 155

<210> 269

<211> 159

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(478)

<223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787

<400> 269

Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln
1 5 10 15

Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His
20 25 30

Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
35 40 45

Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu
50 55 60

Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser
65 70 75 80

Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala
85 90 95

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys
 100 105 110

Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe
 115 120 125

Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
 130 135 140

Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu
 145 150 155

<210> 270

<211> 487

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 270

t gtg gcc atc tgc aaa cct ctt cat tac aca acc atc att agc acc agg 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
 1 5 10 15

gtt tgt atc ctt ctt gtc tgt agc tcc tgg ctt gca gga ttc ttg atc 97
 Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
 20 25 30

atc ttt cca cca ata atc ctt ctt ctg cag ttg gac ttc tgt gcc tcc 145
 Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
 35 40 45

aat ata att gat cat ttt atc tgt gat tct tct cca att ctg cag ctt 193
 Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
 50 55 60

tct tgt aca aac act cac ttt cta gaa ctc atg gca ttt tgt tta gcc 241
 Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
 65 70 75 80

gtg gtg aca ctc atg gtc acc ttg acc tta gtt att ctc tcc tat aca 289
 Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
 85 90 95


```

aat att atc cgg aca att cta aga att cct tct atg agt caa agg aaa      337
Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
      100                      105                      110

aaa gcc ttt tcc act tgt tcc tcc cat ata ata gtt gtt tcc ctg tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
      115                      120                      125

tat ggt agt tgt atc ttc atg tac ata aag cct tct aca agg gaa agg      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
      130                      135                      140

gtg act tta agc aaa gga gta gct gtg gtt aat act tca gtg gct cct      481
Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
      145                      150                      155                      160

ctt ttg
Leu Leu
      487

```

```

<210> 271
<211> 162
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788
<400> 271
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
1                      5                      10                      15

```

```

Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
      20                      25                      30

```

```

Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
      35                      40                      45

```

```

Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
      50                      55                      60

```

```

Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
      65                      70                      75                      80

```

```

Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
      85                      90                      95

```

Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
 130 135 140

Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
 145 150 155 160

Leu Leu

<210> 272
 <211> 483
 <212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(483)
 <223> Taxon = 34829; gene = ERU165; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF179789
 <400> 272

cgttgccatc tgcaagcccc tccactaccc ccgtgctcat gagcagcagg gtctgcacac 60
 agctcatcct cgcctgctgg ctggcagggt tctccttcat cattgtgcct gtcacacctga 120
 ccagtcagct tccattctgt gacaccacaca tcaaccactt cttctgtgac tatacacctc 180
 taatggagggt ggtctgcagt gggccaaagg tgctggagat ggtggatttt accctggcct 240
 tgggtggcact gctcagcacc ttggtgctga tcaccctgtc ctacatccag atcatcagga 300
 cgattgtcag gatccctctt gtccaggaga ggaaaaaggc tttctccacc tgttctctcc 360
 atgtcatcgt ggttaccatg tgctatggaa gctgtttttt tatgtatgtc aagccctccc 420
 caggcaaagg gggtgatcta aacaaaggag tgtcttaatc aatacaatta ttgccccctt 480
 ctt 483

<210> 273
 <211> 486
 <212> DNA
 <213> Eulemur rubriventer
 <220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 34829; gene = ERU167; Accession DDBJ/EMBL/GenBank = AF179790

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 273

```

t  gtg gcc atc tgt cac cct ctg aga tac aca gac atc atg act cct cgt      49
   Val Ala Ile Cys His Pro Leu Arg Tyr Thr Asp Ile Met Thr Pro Arg
   1              5              10              15

```

```

ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat      97
Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
   20              25              30

```

```

gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac      145
Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
   35              40              45

```

```

ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc      193
Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
   50              55              60

```

```

gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct      241
Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
   65              70              75              80

```

```

tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act      289
Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
   85              90              95

```

```

caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat      337
Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
   100             105             110

```

```

aaa gcc ttt tcc acc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
   115             120             125

```

```

tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct      433
Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
   130             135             140

```

```

tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc      481
Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
   145             150             155             160

```

```

tgt tg      486
Cys

```

<210> 274

<211> 161
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 34829; gene = ERU167; Accession DDBJ/EMBL/GenBank = AF179790
<400> 274

Val Ala Ile Cys His Pro Leu Arg Tyr Thr Asp Ile Met Thr Pro Arg
1 5 10 15

Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
20 25 30

Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
35 40 45

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
50 55 60

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
65 70 75 80

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
85 90 95

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
130 135 140

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
145 150 155 160

Cys

<210> 275

```

<211> 487
<212> DNA
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU168; Accession DDBJ/EMBL/GenBank = AF179791
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 275
t gtg gcc atc tgt cac cct ctg aca tac aca gac atc atg act cct cgt      49
  Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg
    1             5             10             15

ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat      97
  Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
        20             25             30

gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac      145
  Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
        35             40             45

ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc      193
  Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
    50             55             60

gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct      241
  Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
    65             70             75             80

tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act      289
  Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
        85             90             95

caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat      337
  Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
        100            105            110

aaa gcc ttt tcc gcc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc      385
  Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
        115            120            125

tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct      433
  Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
        130            135            140

tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc      481
  Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
    145            150            155            160

gtg ttg
Val Leu

```

<210> 276
<211> 162
<212> PRT
<213> Eulemur rubriventer
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU168; Accession DDBJ/EMBL/GenBank = AF179791
<400> 276

Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg
1 5 10 15

Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
20 25 30

Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
35 40 45

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
50 55 60

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
65 70 75 80

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
85 90 95

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
100 105 110

Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
130 135 140

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
145 150 155 160

Val Leu

```

<210> 277
<211> 486
<212> DNA
<213> Macaca sylvanus
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792
<220>
<221> CDS
<222> (1)..(486)
<223> Product = olfactory receptor
<400> 277
cct gcc atc tgc cag cca ctc agg tac cgc gtg ctc atg aac cac cgg      48
Pro Ala Ile Cys Gln Pro Leu Arg Tyr Arg Val Leu Met Asn His Arg
1              5              10              15

ctc tgt gtg ctg ctg gtg gga gct gcc tgg gtc ctc tgc ctc ctc aag      96
Leu Cys Val Leu Leu Val Gly Ala Ala Trp Val Leu Cys Leu Leu Lys
20              25              30

tcg gtg act gag aca gtc att gcc atg agg ctg ccc ttc tgt ggc cac      144
Ser Val Thr Glu Thr Val Ile Ala Met Arg Leu Pro Phe Cys Gly His
35              40              45

cac gtg gtc agt cac ttc acc tgc gag atc ctg gcg gtg ctg aag ctg      192
His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu
50              55              60

acg tgc ggt aac aca tcg gtc agc gag gtc ttc ctg ctg gtg ggc tcc      240
Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser
65              70              75              80

atc ctg ctg ctg cct gtg ccc ctg gca ttc att tgc ctg tcc tac ttg      288
Ile Leu Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu
85              90              95

ctc atc ctg gcc acc atc ctg agg gtg ccc tca gct gct ggg tgc cgc      336
Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg
100             105             110

aaa gcc ttc tcc acc tgc tca gca cac ctg gct gtg gtg ctg ctt ttc      384
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe
115             120             125

tac agc acc atc atc ttc acg tac atg aag ccc aag agc aag gaa gcc      432
Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala
130             135             140

cac atc tot gat gag gtc ttc aca gtc ctc tac gcc atg gtc aca ccc      480
His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro
145             150             155             160

```

atg ttg
Met Leu

486

<210> 278
<211> 162
<212> PRT
<213> *Macaca sylvanus*
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792
<400> 278

Pro Ala Ile Cys Gln Pro Leu Arg Tyr Arg Val Leu Met Asn His Arg
1 5 10 15

Leu Cys Val Leu Leu Val Gly Ala Ala Trp Val Leu Cys Leu Leu Lys
20 25 30

Ser Val Thr Glu Thr Val Ile Ala Met Arg Leu Pro Phe Cys Gly His
35 40 45

His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu
50 55 60

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser
65 70 75 80

Ile Leu Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu
85 90 95

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe
115 120 125

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala
130 135 140

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro
145 150 155 160

Met Leu

<210> 279
 <211> 489
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(489)
 <223> Taxon = 9546; gene = MSY173; pseudogene; Accession DDBJ/EMBL/GenBank = AF179793
 <400> 279
 cgtggccatc tgtaaccac tgtgtgtacac gggtcaccatg tctccccaga tgtgtttgct 60
 cctttttgctg ggtgtctatg ggatgggggt ttttggggct gtgactcata tgggaaacat 120
 aacgtttatg tcctttttgtg gagacaacct tgtcaatcac tacatgtgtg acctccttcc 180
 tctccttgag ctctcttgca acagcactta cataaatttg ctgggtggtt ttattattgt 240
 gaccaatggc attgggggtgc caattgtcac cattttttatc tcttatgggt ttattctttc 300
 cagcattctc cacattagct ccacagaggg caggtctaaa gccttcagta cctgcagttc 360
 cacataattg tgggtatcgt gttcttttggg tcaggtgctt tcatgtacct cacaccacct 420
 tctagtctac ccctggacca ggggaacgtg tcctccattt ttatactgc tgtaatgccc 480
 atgtagatt 489

<210> 280
 <211> 481
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(4818)
 <223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794
 <220>
 <221> CDS
 <222> (2)..(481)
 <223> product = olfactory receptor
 <400> 280
 t gtg gcc atc tgt aag ccc ttg cac tat gca acc atc atg agt caa cct 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 1 5 10 15
 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat 97
 Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
 20 25 30

gga ggg atc cag act ttg ttc ata gcc cac tta cca ttc tgt ggc cct 145
 Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
 35 40 45

aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg 193
 Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 50 55 60

gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt 241
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 65 70 75 80

gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc 289
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 85 90 95

atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa 337
 Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
 100 105 110

gtt ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt 385
 Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
 115 120 125

gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ttc ccc 433
 Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
 130 135 140

act gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg 481
 Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
 145 150 155 160

<210> 281

<211> 160

<212> PRT

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(4818)

<223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794

<400> 281

Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 1 5 10 15

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
 20 25 30

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
 35 40 45

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 50 55 60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 65 70 75 80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 85 90 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
 100 105 110

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
 115 120 125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
 130 135 140

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
 145 150 155 160

<210> 282

<211> 402

<212> DNA

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(402)

<223> Taxon = 9546; gene = MSY175; pseudogene; Accession DDBJ/EMBL/GenBank = AF179795

<400> 282

tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcatgca 60

gcttgtgctt ggggtgttggc ttgctgggtt ctcgtcacct ttccaccact cctcttaggc 120

ctaaatcttg acttctgtgc ctgcctccaa cgtcattaat catttctact gtgacactac 180

tccactcctg cagatttcct gcactgacac acagctcctg gacaggatgg gattcatttc 240

agcattgggtg acactcttag tcacattgggt aatgggtgatg gtatcatgat atccctttct 300

tatggcagtt gcattctcat gtatgttaag ccacgggtca aacaaaagat atatttttca 360

aagggaattt tgggtgctcaa cacctctgtc gttccacttt tg 402

<210> 283
 <211> 487
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 283

c	gtg	gct	att	tgc	aac	cct	ctg	ctc	tac	gca	tta	gtg	gtg	tct	cca	aag	49
	Val	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Ala	Leu	Val	Val	Ser	Pro	Lys	
1				5					10					15			
gta	tgt	cgt	ctg	ctg	gtg	tcc	ctc	aca	tac	ctt	cag	agt	ctt	atc	aca		97
Val	Cys	Arg	Leu	Leu	Val	Ser	Leu	Thr	Tyr	Leu	Gln	Ser	Leu	Ile	Thr		
		20						25					30				
gcc	ctt	act	gtc	tct	tcc	tgt	gtg	ttc	tct	gtg	tca	tac	tgt	tct	tcc		145
Ala	Leu	Thr	Val	Ser	Ser	Cys	Val	Phe	Ser	Val	Ser	Tyr	Cys	Ser	Ser		
		35					40					45					
aac	atc	atc	aac	cat	ttt	tac	tgt	gac	gat	gtc	cct	ttg	cta	gca	ttg		193
Asn	Ile	Ile	Asn	His	Phe	Tyr	Cys	Asp	Asp	Val	Pro	Leu	Leu	Ala	Leu		
	50				55					60							
tcg	tgt	tct	gat	acc	tac	att	cca	gaa	aca	gca	gtg	ttt	atc	ttt	tca		241
Ser	Cys	Ser	Asp	Thr	Tyr	Ile	Pro	Glu	Thr	Ala	Val	Phe	Ile	Phe	Ser		
65				70					75				80				
ggg	acc	aat	ttg	ttt	ttc	tcc	atg	acc	gtt	ggt	ctg	ata	tcc	tac	ttc		289
Gly	Thr	Asn	Leu	Phe	Phe	Ser	Met	Thr	Val	Val	Leu	Ile	Ser	Tyr	Phe		
			85					90					95				
aac	att	ggt	att	acc	att	ttg	agg	ata	cgt	tcc	tca	gaa	gga	cga	caa		337
Asn	Ile	Val	Ile	Thr	Ile	Leu	Arg	Ile	Arg	Ser	Ser	Glu	Gly	Arg	Gln		
		100					105						110				
aaa	gcc	ttt	tcc	acg	tgt	gct	tct	cac	atg	ata	gct	gtg	ggt	gtg	ttc		385
Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Met	Ile	Ala	Val	Val	Val	Phe		
		115				120					125						
tat	ggg	act	ctc	ctt	ttc	atg	tat	ttg	caa	cca	agg	agt	aat	cac	tca		433
Tyr	Gly	Thr	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Arg	Ser	Asn	His	Ser		
	130				135					140							
tta	gat	act	gac	aaa	atg	gcc	tcg	gtc	ttc	tac	acc	ctg	atc	ata	cct		481
Leu	Asp	Thr	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Ile	Ile	Pro		
145				150					155				160				

atg ttg
Met Leu

487

<210> 284
<211> 162
<212> PRT
<213> Macaca sylvanus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796
<400> 284

Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
1 5 10 15

Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
20 25 30

Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
35 40 45

Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
50 55 60

Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
65 70 75 80

Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
85 90 95

Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val Phe
115 120 125

Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
145 150 155 160

Met Leu

```

<210> 285
<211> 487
<212> DNA
<213> Macaca sylvanus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 285
t  gtg gcc atc tgt cac cct cta cat tat gcc atc atc atg ggt cag agt      49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
    1              5              10              15

cag tgt gtc acg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt      97
  Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
    20              25              30

gct ctt ttg cac act ctc ctc ctg gcc tgg ctt tcc ttc tgt gct gat      145
  Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
    35              40              45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg      193
  His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
    50              55              60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga      241
  Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
    65              70              75              80

ttg aca gcc att atg ctt cca ttc ctg tgt atc ctg gtt tct tat ggt      289
  Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
    85              90              95

cac act gca gtc acc atc ctc cag att ccc tct act aat ggc ata tgc      337
  His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
    100             105             110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gca gtg act ctc tat      385
  Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
    115             120             125

tat ggg acc att att ggt ctc tat ttt ctt ccc cca tcc agc aac act      433
  Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
    130             135             140

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aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 481
 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ttg 487
 Met Leu

<210> 286
 <211> 162
 <212> PRT
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797
 <400> 286

Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
 1 5 10 15

Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 287
 <211> 487
 <212> DNA
 <213> Macaca sylvanus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> product = olfactory receptor
 <400> 287

t	gtg	gcc	atc	tgc	ttc	ccc	ctg	cac	tac	acc	gcc	atc	atg	agc	ccc	atg	49
	Val	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Thr	Ala	Ile	Met	Ser	Pro	Met	
1				5					10					15			
ctc	tgt	ctc	gcc	ctg	gtg	gcg	ctg	tcc	tgg	gta	ctg	acc	acc	ttc	cat	97	
Leu	Cys	Leu	Ala	Leu	Val	Ala	Leu	Ser	Trp	Val	Leu	Thr	Thr	Phe	His		
	20							25					30				
gcc	atg	tta	cac	act	tta	ctc	atg	gcc	agg	ttg	tgt	ttt	tgt	gca	gac	145	
Ala	Met	Leu	His	Thr	Leu	Leu	Met	Ala	Arg	Leu	Cys	Phe	Cys	Ala	Asp		
	35						40				45						
aat	gtg	atc	ccc	cac	ttt	ttc	tgt	gat	atg	tct	gct	ctg	ctg	aag	ctg	193	
Asn	Val	Ile	Pro	His	Phe	Phe	Cys	Asp	Met	Ser	Ala	Leu	Leu	Lys	Leu		
	50					55				60							
gcc	tgc	tct	gac	act	caa	gtt	aat	gaa	ttg	gcg	ata	ttt	atc	acg	gga	241	
Ala	Cys	Ser	Asp	Thr	Gln	Val	Asn	Glu	Leu	Ala	Ile	Phe	Ile	Thr	Gly		
65				70				75				80					
ggg	ctg	att	ctt	gtc	atc	cca	ttc	cta	ctc	atc	ctt	ggg	tcc	tat	gca	289	
Gly	Leu	Ile	Leu	Val	Ile	Pro	Phe	Leu	Leu	Ile	Leu	Gly	Ser	Tyr	Ala		
	85					90						95					
cgg	att	gtc	tcc	tcc	atc	ctc	aag	gtc	cct	tcg	tct	aag	ggt	atc	tgc	337	
Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys	Val	Pro	Ser	Ser	Lys	Gly	Ile	Cys		
	100					105						110					
aag	gcc	ttc	tct	act	tgt	ggc	tcc	cac	ctc	tct	gtg	gtg	tca	ctg	ttc	385	
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe		
	115					120					125						
tat	ggg	acc	gtt	att	ggt	ctc	tac	ttc	tgc	cca	tca	gct	aat	agt	tct	433	

Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
 130 135 140

act cta aag gag act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 288

<211> 162

<212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

<400> 288

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly
 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser

130

135

140

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 289

<211> 484

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9546; gene = MSY179; Accession DDBJ/EMBL/GenBank = AF179799

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 289

a tgt gcc atc tgc tgc ccc ctc cac tac acc aca gcc atg agc cct aag 49
 Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys
 1 5 10 15

ctc tgt atc tta ctc ctt tcc ttg tgt tgg gtc tta tct gtg ctc tat 97
 Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr
 20 25 30

ggc ctc ata cac acc ttc ctc atg acc acg gtg acc ttc tgt ggg tca 145
 Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser
 35 40 45

cga aaa atc cac tac atc ttc tgt gag atg tat gta ttg ctg agg ctg 193
 Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu
 50 55 60

gca tgt tcc gac act cag att aat cac aca gtg ctg att gcc aca ggc 241
 Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly
 65 70 75 80

tgc ttt atc ttc ctc att ccc ttt gga ttc atg atc att tcc tat gtg 289
 Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val
 85 90 95

ttg att gtc aga gcc atc ctc aga ata ccc tca gtc tct aag aaa tac 337
 Leu Ile Val Arg Ala Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr
 100 105 110

aaa gcc ttc tcc act tgt gcc tcc cat ttg ggt gta gtc tcc ctc ttc 385
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Gly Val Val Ser Leu Phe

115	120	125	
tat ggg aca ctt tgt atg gta tac ctg aag ccc ctc cat acc tac tct			433
Tyr Gly Thr Leu Cys Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser			
130	135	140	
gtg aag gac tca gta gcc aca gtg atg tat gcg gtg gtg aca ccc atg			481
Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met			
145	150	155	160
atg			484
Met			
<210>	290		
<211>	161		
<212>	PRT		
<213>	Macaca sylvanus		
<220>			
<221>	misc_feature		
<222>	(1)..(484)		
<223>	Taxon = 9546; gene = MSY179; Accession DDBJ/EMBL/GenBank = AF179799		
<400>	290		
Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys			
1	5	10	15
Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr			
	20	25	30
Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser			
	35	40	45
Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu			
	50	55	60
Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly			
	65	70	75
			80
Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val			
	85	90	95
Leu Ile Val Arg Ala Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr			
	100	105	110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Gly Val Val Ser Leu Phe			
	115	120	125

Tyr Gly Thr Leu Cys Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser
 130 135 140

Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met
 145 150 155 160

Met

<210> 291
 <211> 487
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY180; pseudogene; Accession DDBJ/EMBL/GenBank = AF179800
 <400> 291
 tgctgccata tgtcaccctc tccattacac tgccatcatg aggggaagagc tctgtgtctt 60
 cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct 120
 gaccagctg tctttctgtg ctgcgaacac catccccac atcttctgtg accttgctgc 180
 cctgtcgaag ctgtcctggg cagatatctt cctcaatgag ctgggtcatgt tcacagtagg 240
 ggtggtgggc attaccctgc cattcatgtg taccctggta tcatatggct aactgggggc 300
 caccatcctg aggggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc 360
 ccatctctct gtgggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac 420
 tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc 480
 cgtgttg 487

<210> 292
 <211> 487
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY181; pseudogene; Accession DDBJ/EMBL/GenBank = AF179801
 <400> 292

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tgctgccata tgtcaccctc tccattacac tgccatcatg aggggaagagc tctgtgtctt    60
cttagtgggt gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cccttctcct    120
gaccagctg tctttctgtg ctgcgaacac catccccac atcttctgtg accttgctgc    180
cctgctcaag ctgtcctggg cagatatctc cctcaatgag ctggatcatgt tcacagtagg    240
gggtggtggc attaccctgc cattcatgtg tatcctggta tcatatggct aactggggc    300
caccatcctg aggggccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc    360
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac    420
tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc    480
cgtgttg                                           487

```

<210> 293

<211> 487

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 293

```

t gtg gcc atc tgt aaa ccc ctt cat tat atg gtc atc atg aac aac agg    49
  Val Ala Ile Cys Lys Pro Leu His Tyr Met Val Ile Met Asn Asn Arg
    1             5             10            15

```

```

gtg tgt acc tta tta gtc ctc tgc agt tgg gtg gct ggc ttg atg atc    97
  Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
          20             25             30

```

```

att gtt cca cca ctg agc tta ggc ctc cag ctc gaa ttc tgt ggc tcc    145
  Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
          35             40             45

```

```

aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc    193
  Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
    50             55             60

```

```

tca tgc tca gac aca tgg gta ata gaa cag ata gtt ata ctt atg gct    241
  Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
    65             70             75             80

```

```

gta ttt gca ctc att atc acc cta gtt tgt gtg att ctg tcc tac ttg    289
  Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu

```

	85		90		95	
tac ata gtc aga aca att ctg agg ttc cct tct gtt cag caa agg aaa						337
Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys						
	100		105		110	
aag gcc ttt tct acc tgt tca tcc cac atg att gtg gtt tcc att gcc						385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala						
	115		120		125	
tat gga agc tgc atc ttc gtc tat atc aag ccc tct gca aaa gat gaa						433
Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu						
	130		135		140	
gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtt gca ccc						481
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro						
	145		150		155	160
ttg ttg						487
Leu Leu						

```
<210> 294
<211> 162
<212> PRT
<213> Macaca sylvanus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802
<400> 294
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Val Ala Ile Cys Lys Pro Leu His Tyr Met Val Ile Met Asn Asn Arg
1 5 10 15

Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
20 25 30

Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
35 40 45

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
50 55 60

Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
65 70 75 80

Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
85 90 95

Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
 115 120 125

Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 130 135 140

Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
 145 150 155 160

Leu Leu

<210> 295

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 295

t gtg gcc att tgc cgc ccc ctg tac tac tcc aca gtc atg agc ccc caa 49
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
 1 5 10 15

gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt 97
 Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
 20 25 30

gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act 145
 Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45

ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta 193
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60

tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga 241
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80

```

ggc aca gta ctc att gtc ccc ttt ata tgc att gtc acc tcc tac atc      289
Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
      85                      90                      95

cac att gtg cct gct atc ctg agg gtc cga acc tgt ggt ggg gcg ggc      337
His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
      100                    105                    110

aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt ata ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
      115                    120                    125

tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tct att gcc tct      433
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
      130                    135                    140

gaa gag aag gac att gca gca gct gca ctg tat acc ata gtg act ccc      481
Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
      145                    150                    155                    160

atg ttg      487
Met Leu

```

```

<210> 296
<211> 162
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803
<400> 296
Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
1          5          10          15

```

```

Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
      20          25          30

```

```

Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
      35          40          45

```

```

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
      50          55          60

```

```

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
      65          70          75          80

```


Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
85 90 95

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130 135 140

Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
145 150 155 160

Met Leu

<210> 297

<211> 486

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/GenBank = AF179804

<220>

<221> CDS

<222> (1)..(486)

<223> Product = olfactory receptor

<400> 297

gtg gcc atc tgt cac cca ctg cac tac aca gtc acc att aac ccc aga 48
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1 5 10 15

ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 96
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20 25 30

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac 144
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

ttg gaa atc ccc cgc ttt ttc tgc gaa ctt aat cag gtc atc cac ctt 192
Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50 55 60

```

gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gct      240
Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
65                      70                      75                      80

gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tct      288
Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
                        85                      90                      95

aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac      336
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
                        100                     105                     110

aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta ttt      384
Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
                        115                     120                     125

tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac      432
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
                        130                     135                     140

tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc ccc      480
Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
145                     150                     155                     160

atg ctg
Met Leu
486

```

<210> 298

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/ GenBank = AF179804

<400> 298

```

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1                      5                      10                      15

```

```

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20                      25                      30

```

```

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
35                      40                      45

```

```

Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50                      55                      60

```

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
65 70 75 80

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 299

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 299

c gtg gcc atc tgt aac cca ctg ttg tac atg gtc acc atg tct ccc cag 49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1 5 10 15

gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gct ttg ggg 97
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly
20 25 30

gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt gca gaa 145
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu
35 40 45

acc ctt gtc aat cac tac atg tgt gac atc ctt ccc ctc ctt gag ctc 193

```

Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
 50                      55                      60

tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg      241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val
65                      70                      75                      80

acc att ggc att ggg gtg ccc att gtc acc att ttt atc tct tat ggt      289
Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
                        85                      90                      95

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser
                        100                      105                      110

aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Leu Leu Phe
                        115                      120                      125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
                        130                      135                      140

ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc      481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
145                      150                      155                      160

atg ttt
Met Phe
                                         487

```

```

<210> 300
<211> 162
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805
<400> 300

```

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1                      5                      10                      15

```

```

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly
20                      25                      30

```

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu
35                      40                      45

```

```

Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu

```

[illegible]

```

<210> 301
<211> 487
<212> DNA
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9483; gene = CJA196; Accession DDBJ/EMBL/GenBank = AF179806
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 301
c ttg gcc atc tgc cac ccg ctg cac tac tcc tcc aag atg agc ctg tgc          49
  Leu Ala Ile Cys His Pro Leu His Tyr Ser Ser Lys Met Ser Leu Cys
    1                      5                      10                      15

agc tgc acc cta atg ttg ggc tgc tta tgg acc act gcc agc ctc cat          97
Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His
      20                      25                      30

gcc ctt ctg cac acc ctt ctc ttg gcc cgg ctg gac ttc tgt gcc agc          145
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser

```

PCT/IB00/02017

Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser
35 40 45

Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu
 50 55 60

Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly
 65 70 75 80

Gly Leu Ile Ile Leu Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr
 85 90 95

Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe
 115 120 125

Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser Ser His Ser
 130 135 140

Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 303
 <211> 487
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 303
 t gtt gcc ata tgt cac cca ctg cac tac aca gtc acc att aac ccc aga 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
 1 5 10 15
 ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 97
 Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
 20 25 30

```

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac      145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
      35                      40                      45

ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc atc cac ctt      193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
      50                      55                      60

gcc tgt tct gac act ttt ctt aat gat gtg gtg atg tat ttg gcc gct      241
Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
      65                      70                      75                      80

gtg ctg ctg ggg ggt ggt ccc ctt gca ggg att ctt tac tct tac tct      289
Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
      85                      90                      95

aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac      337
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
      100                      105                      110

aag gca ttt tcc acc tgt gta tct cac atc tta att gtc tcc tta ttt      385
Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
      115                      120                      125

tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac      433
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
      130                      135                      140

tca cat tca aga gct gca gcc tcg gtg atg tac act gtg gtc acc ccc      481
Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
      145                      150                      155                      160

atg ctg      487
Met Leu

```

<210> 304

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807

<400> 304

```

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1                      5                      10                      15

```

```

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20                      25                      30

```


Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
 35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
 50 55 60

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
 65 70 75 80

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
 100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 305

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 305

c att gcc atc tgt agc ccc ttg ctg tac aat gtc atc atg tcc tat cac 49
 Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His
 1 5 10 15

```

ttc tgc ttc cgg ctc aca gtg gga gtt tac att tta ggc atc ctt gga      97
Phe Cys Phe Arg Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly
      20                      25                      30

tct aca att cac acc agc tct atg ttg aga ctc ttt ctg tgc aaa act      145
Ser Thr Ile His Thr Ser Ser Met Leu Arg Leu Phe Leu Cys Lys Thr
      35                      40                      45

aat gtg att aac cat tat ttt tgt gat ctc ttc cct ctc ttg gaa ctc      193
Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu
      50                      55                      60

tcc tgc tcc agt acc tac atc aat gaa tta cta gtt ctg gtc ttg agt      241
Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser
      65                      70                      75                      80

gca ttg aat atc ctg acg cct gcc tta act atc ctg gcc tct tat atc      289
Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile
      85                      90                      95

ttc acc att gcc agt atc ctc cac att cgc tcc act gag ggc agg tcc      337
Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser
      100                      105                      110

aaa gcc ttc agc act tgc agc tcc cac atc tca gct gtt gct gtc ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe
      115                      120                      125

ttt gga tct gca gca ttc atg tac ctg cag cca tca tct gtc agt tcc      433
Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser
      130                      135                      140

atg gac cag ggg aaa gtg tca tct gtg ttt tac aca act gtt gtg ccc      481
Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro
      145                      150                      155                      160

atg ctg      487
Met Leu

```

<210> 306

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<400> 306

```

Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His
1           5           10           15

```

Phe Cys Phe Arg Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly
20 25 30

Ser Thr Ile His Thr Ser Ser Met Leu Arg Leu Phe Leu Cys Lys Thr
35 40 45

Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu
50 55 60

Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser
65 70 75 80

Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile
85 90 95

Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe
115 120 125

Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser
130 135 140

Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro
145 150 155 160

Met Leu

<210> 307

<211> 469

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(469)

<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809

<220>

<221> CDS

<222> (2)..(469)

<223> Product = olfactory receptor

<400> 307

```

t gtt gct atc tgt cac ccc ctg cac tac acc act gtc atg agt cgg gga      49
Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly
1           5           10           15

tta tgc tgt gtg ttg gtt gct gcc tcc tgg atg gga gga ttt gtg cac      97
Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His
          20           25           30

tcc acc gtc cag acc att ctc act atc cgt ctg ccc ttt tgt ggg cca      145
Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro
          35           40           45

aat cag gtg gac aac ttt ttt tgt gat gtt ccc cct gtc atc aaa ctt      193
Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu
          50           55           60

gcc tgt gct gac act ttt gtc att gaa ttg ctc atg gta tct aac agt      241
Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Met Val Ser Asn Ser
65           70           75           80

ggg ttg atc tcc acc agc tcc ttt gtg gtg ctg att tcc tcc tac acc      289
Gly Leu Ile Ser Thr Ser Ser Phe Val Val Leu Ile Ser Ser Tyr Thr
          85           90           95

act atc cta gtc aag att cac tcc aag gag gga agg cga aag gca ctc      337
Thr Ile Leu Val Lys Ile His Ser Lys Glu Gly Arg Arg Lys Ala Leu
          100          105          110

tcc aca tgt gcc tct cac ctt atg gtg gta aca ctt ttt gga ccc tgt      385
Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Gly Pro Cys
          115          120          125

agt ttc atc tat cct cat cct ttc tct aca ttt tct gtg gac aag atg      433
Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met
          130          135          140

gtg tct gta ctc tac aag gtt att act cca atg cta      469
Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu
145          150          155

```

<210> 308

<211> 156

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(469)

<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809

<400> 308

```

Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly
1           5           10           15

```

Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His
 20 25 30

Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro
 35 40 45

Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu
 50 55 60

Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met Val Ser Asn Ser
 65 70 75 80

Gly Leu Ile Ser Thr Ser Ser Phe Val Val Leu Ile Ser Ser Tyr Thr
 85 90 95

Thr Ile Leu Val Lys Ile His Ser Lys Glu Gly Arg Arg Lys Ala Leu
 100 105 110

Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Gly Pro Cys
 115 120 125

Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met
 130 135 140

Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu
 145 150 155

<210> 309

<211> 488

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 309

c gtt gcc att tgc ttc ccc ctt cgc tat atg cta ctc atg agc cat tcc 49
 Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser
 1 5 10 15

att tgt gtc acg atg att ata gtt tgt tgg tcc att agc ata gct ggg 97

310

```

Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
      20              25              30

gcc ctg atc ctc act gtc ttc acc atg cat ctg cct tat tgt ggc ccc      145
Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro
      35              40              45

tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg      193
Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
      50              55              60

gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc atc ttg ggt      241
Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
      65              70              75              80

ttc atc ctg ctt ttg gtc cca ctc tcc ctc atc ctg gcc tct tac gtc      289
Phe Ile Leu Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val
      85              90              95

ttc atc ttt gcc tct atc ttc aga atc cgc tca gcg cag ggg agg ctc      337
Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu
      100              105              110

aag tcc ttc tcc acg tgt gct tcc cac gtc act gtg gtc acc atg ttc      385
Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
      115              120              125

tat ggg ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac      433
Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
      130              135              140

cca gag cgg gac aag aag cta gcg ctg ttc tac aat gtg gtc tct ggc      481
Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly
      145              150              155              160

ttc ctc a
Phe Leu
      488

```

<210> 310

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

<400> 310

```

Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser
1              5              10              15

```

Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
 20 25 30

Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro
 35 40 45

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
 50 55 60

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
 65 70 75 80

Phe Ile Leu Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val
 85 90 95

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu
 100 105 110

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
 115 120 125

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
 130 135 140

Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly
 145 150 155 160

Phe Leu

<210> 311
 <211> 487
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 311
 t gtg gca att tgc cac ccc tta cgt tac act gcc aca atg aac ctg cgc 49

Val	Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Thr	Ala	Thr	Met	Asn	Leu	Arg	
1				5					10					15		
ctt	tgt	gtc	cag	cta	gtg	gct	gga	ctg	tgg	ctt	gtt	act	tac	ctc	cat	97
Leu	Cys	Val	Gln	Leu	Val	Ala	Gly	Leu	Trp	Leu	Val	Thr	Tyr	Leu	His	
		20					25				30					
gcc	ctc	ctg	cat	act	tcc	cta	ata	gca	cat	ctg	tcc	ttc	tgt	gcc	ttc	145
Ala	Leu	Leu	His	Thr	Ser	Leu	Ile	Ala	His	Leu	Ser	Phe	Cys	Ala	Phe	
		35				40				45						
aat	atc	atc	cat	cat	ttc	ttc	tgt	gat	ctc	aac	cct	cta	cta	cgg	ctc	193
Asn	Ile	Ile	His	His	Phe	Phe	Cys	Asp	Leu	Asn	Pro	Leu	Leu	Arg	Leu	
	50				55				60							
tct	tgc	tct	gcc	gtc	tcc	ttc	aac	gta	atg	atc	att	ttt	gca	gta	gga	241
Ser	Cys	Ser	Ala	Val	Ser	Phe	Asn	Val	Met	Ile	Ile	Phe	Ala	Val	Gly	
65				70				75					80			
ggt	cta	ttg	gct	ctc	acg	ccc	ctt	gtc	tgt	atc	ctc	gta	ttt	tat	gga	289
Gly	Leu	Leu	Ala	Leu	Thr	Pro	Leu	Val	Cys	Ile	Leu	Val	Phe	Tyr	Gly	
			85					90					95			
ctt	atc	ttc	tcc	act	gtt	ctg	aag	atc	acc	tct	act	cag	ggg	aaa	cag	337
Leu	Ile	Phe	Ser	Thr	Val	Leu	Lys	Ile	Thr	Ser	Thr	Gln	Gly	Lys	Gln	
		100				105						110				
aga	gct	gct	tcc	acc	tgc	ggc	tgc	cac	ctg	tca	gta	gtg	gtg	ctg	ttt	385
Arg	Ala	Ala	Ser	Thr	Cys	Gly	Cys	His	Leu	Ser	Val	Val	Val	Leu	Phe	
		115				120					125					
tat	ggc	aca	gcc	att	gcc	gtc	tac	ttt	agc	ccc	tca	tcc	tcc	cat	acg	433
Tyr	Gly	Thr	Ala	Ile	Ala	Val	Tyr	Phe	Ser	Pro	Ser	Ser	Ser	His	Thr	
	130				135					140						
cct	gag	agt	gac	act	ctc	tcg	acc	gtc	atg	tat	tca	gtg	gtg	gcc	ccg	481
Pro	Glu	Ser	Asp	Thr	Leu	Ser	Thr	Val	Met	Tyr	Ser	Val	Val	Ala	Pro	
145				150					155					160		
atg	ctg															487
Met	Leu															

<210> 312

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811

<400> 312

Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ala Thr Met Asn Leu Arg

WO 01/46262

313

PCT/IB00/02017

```

1           5           10           15

Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
      20           25           30

Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
      35           40           45

Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu
      50           55           60

Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
      65           70           75           80

Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
      85           90           95

Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
      100           105           110

Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Val Leu Phe
      115           120           125

Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Ser His Thr
      130           135           140

Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
      145           150           155           160

Met Leu

```

```

<210> 313
<211> 491
<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(491)
<223> Taxon = 9600; gene = PPY110; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179812
<400> 313
cgtggccatc tgtaaccac tgttgtaaac ggtcacatg tctccccaga tgtgtttgct      60

```

cctttcactg ggtgtctatg ggatgggggt ttttggggct gtggttcata tgggaaacat 120
aatgtttatg tccttttgtg gagacaacct tgtcaatcac tatctgtgtg acatccttcc 180
tctccttgag ctctcctgca acagctctta cataaatttg ctggtgggtt ttattattgt 240
gaccattggc attgggggtgc caattgtcac catttttatc tcttatgggtt ttattctttc 300
cagcattctc cacattagct cacagagggc aggtcaggtc taaagccttc agtacctgca 360
gttccacat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac 420
caccttctct tctaccctg gaccagggga aagtgtcctc cattttttat actgctgtgg 480
tgcccatgtt t 491

<210> 314

<211> 480

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(480)

<223> Taxon = 9600; gene = PPY111; pseudogene; Accession DDBJ/EMBL/GenBank = AF179813

<400> 314

tgtggccatc tgcttcccc tgcactacac catccatcat gagcccatg ctctgtctct 60
cccttttggc gctgtcctgg gtgctgacca ccttccatgc catgttacac actttactca 120
tggccagggt gtgtttttgt gcagacaatg tgatccccc ctttttctgt gatatgtctg 180
ctctgtctgaa gctgtcctgc tctgacactc gagttaatga attgggtgata tttatcatgg 240
gagggctcat tcttgtcatc ccattcctac tcatccttgg gtccatgca cgaattgtct 300
cctccatcct caaggtccct tctaagggtg tctgcaaggc cttctctact tgtggctccc 360
acctctctgt ggtgtccctg ttctatggga ccgtagtggt tctctactta tgcccatcgg 420
ctaatagttc tactctgaag gagactgtca tggctgtaat gtacactgtg gtgaccccca 480

<210> 315

<211> 486

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814

<220>

<221> CDS

<222> (1)..(486)

<223> Product = olfactory receptor

<400> 315

tgt gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc	48
Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser	
1 5 10 15	

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt	96
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys	
20 25 30	

gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac	144
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp	
35 40 45	

cac atc atc tct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ctg	192
His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu	
50 55 60	

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga	240
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly	
65 70 75 80	

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt	288
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly	
85 90 95	

cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc	336
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys	
100 105 110	

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat	384
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr	
115 120 125	

tat ggg aca att att ggt ctc tat ttt cta ccc cca tcc agc aac acc	432
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr	
130 135 140	

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc	480
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro	
145 150 155 160	

atg ttg	486
Met Leu	

<210> 316

<211> 162

<212> PRT

<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814
<400> 316
Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 317
<211> 487
<212> DNA
<213> Pongo pygmaeus
<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9600; gene = PPY113; pseudogene; Accession DDBJ/EMBL/GenBank = AF179815

<400> 317

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cactgccatt tgccaccctc taagataaac caatctcatg agacccaaaa tttgtggact      60
tatgactgcc ttctcctgga tcctgggctc tacggatgga atcattgatg ctgcagcgac    120
attttccttc tcctactgtg ggtctcggga aatagccac ttcttctgtg agttcccttc    180
catactaate ctctcatgca atgacacatc aatatttgaa aaggttcttt tcctctgctg    240
tatagtaatg attgtttttc ctggtgcaat catcatcgct tcctatgctc aagttattct    300
ggctgtcatt cacatgggat ctggagaggg tcgtcggata gctttcacga cctgttcctc    360
tcacctcatg gtggtgggaa tgtactatgg agcagctttg ttcattgtaca tacggccac    420
atctgatcgc tcccctacac aggacaagat ggtgtctgta ttctacacca tcctcactcc    480
catgctg                                           487
```

<210> 318

<211> 484

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

<220>

<221> CDS

<222> (2)..(484)

<223> product = olfactory receptor

<400> 318

```
t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
    1             5             10             15

ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
    20             25             30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
    35             40             45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50             55             60
```

```

tcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga      241
Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65                      70                      75                      80

ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                        85                      90                      95

cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
                        100                     105                     110

gcc ttc tct act tgt ggc tcc cac ctc tct gtg gtg tcc ctg ttc tat      385
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
                        115                     120                     125

ggg acc gtt agt ggt ctc tac tta tgc cca tcg gct aat agt tct act      433
Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
                        130                     135                     140

ctg aag gag act gtc atg gct gta atg tac act gtg gtg acc ccc atg      481
Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
145                      150                      155                      160

ctg      484
Leu

```

<210> 319

<211> 161

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

<400> 319

```

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1                      5                      10                      15

```

```

Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                20                      25                      30

```

```

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
                35                      40                      45

```

```

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50                      55                      60

```

Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
100 105 110

Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
115 120 125

Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
130 135 140

Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
145 150 155 160

Leu

<210> 320

<211> 483

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(483)

<223> Taxon = 9600; gene = PPY115; Accession DDBJ/EMBL/GenBank = AF179817

<220>

<221> CDS

<222> (1)..(483)

<223> Product = olfactory receptor

<400> 320

gtg gcc gtc tgc cac cca ctg cat tac acg ctc atc atg cat gga ggg 48
Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1 5 10 15

ctg tgc ctg ggg ctg gtg gcc ggc tgc ctg gtg gct ggt ttc atg aat 96
Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
20 25 30

tcc ctg atg gaa aca att atc acc ttc cag ctt ctc ctg tgt cac aat 144
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Leu Cys His Asn
35 40 45

gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc 192

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
 50 55 60

tgt gtg gac gtc tcc ttc aac aag gcc atg gtg gcc atc tca ggg ttt 240
 Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe
 65 70 75 80

ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac 288
 Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
 85 90 95

ata gtt gct gcc att ctt cat att cct tct gcc cag gga cgc cgc aaa 336
 Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys
 100 105 110

gcc ttt ggg act tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt 384
 Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
 115 120 125

ggg gct aca atg ttc acc tac atg aga cct gcg ggc ggc tcc tcc ctg 432
 Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
 130 135 140

gaa aag aag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg 480
 Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
 145 150 155 160

ctt 483
 Leu

<210> 321

<211> 161

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(483)

<223> Taxon = 9600; gene = PPY115; Accession DDBJ/EMBL/GenBank = AF179817

<400> 321

Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
 1 5 10 15

Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
 20 25 30

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Leu Cys His Asn
 35 40 45

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala

50

55

60

Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe
65 70 75 80

Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
85 90 95

Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys
100 105 110

Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
115 120 125

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
130 135 140

Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
145 150 155 160

Leu

<210> 322

<211> 484

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY116; Accession DDBJ/EMBL/GenBank = AF179818

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 322

t gtg gcc gtc tgc cac cca ctg cat tac acg ctc atc atg cat gga ggg 49
Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1 5 10 15

ctg tgc ctg ggg ctg gtg gcc ggc tgc ctg gtg gct ggt ttc atg aat 97
Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
20 25 30

tcc ctg atg gaa aca att atc acc ttc cag ctt ccc ctg tgt cac aat 145
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn

35	40	45	
gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc			193
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala			
50	55	60	
tgt gtg gac gtc tcc ttc aac aag gcc acg gtg gcc atc tca ggg ttt			241
Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe			
65	70	75	80
ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac			289
Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His			
85	90	95	
ata gtt gct gcc att ctt cgt att cct tct gcc cag gga cac cgc aaa			337
Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys			
100	105	110	
gcc ttt ggg acc tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt			385
Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe			
115	120	125	
ggg gct aca atg ttc acc tac atg aga cct gcg ggt ggc tcc tcc ctg			433
Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu			
130	135	140	
gaa aag gag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg			481
Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met			
145	150	155	160
ctt			484
Leu			

<210> 323

<211> 161

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY116; Accession DDBJ/EMBL/GenBank = AF179818

<400> 323

Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1 5 10 15

Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
20 25 30

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn
35 40 45

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
 50 55 60

Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe
 65 70 75 80

Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
 85 90 95

Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys
 100 105 110

Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
 115 120 125

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
 130 135 140

Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
 145 150 155 160

Leu

<210> 324

<211> 479

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(479)

<223> Taxon = 9600; gene = PPY117; pseudogene; Accession DDBJ/EMBL/GenBank = AF179819

<400> 324

tgttagccata tgcaaaccct tatactatgt ggtcatcatg agccgaagga cagcactgt 60

cttggtaatg atctcctggg ctgtgggctt ggtgcacaca ttaagccagt tatcatttac 120

tgtgaacctg ccttttttgt ggacctaatg tagtagacag ctttttttgt gatcttcctc 180

gagtgaccaa acttgctgc ctggactctt acctcattga aatactaatt gtggtcaata 240

gtggagtctt ttcctaagc actttctgtc tcttggtcag ctctacatc attattcttg 300

ttatgggtttg gctcaagtct tcggctgcaa tggcgaaggc atttctctacg ctggcttccc 360
 atattgcagt agtaatatta ttctttggac ctgtcatctt catctatgtg tggcccttta 420
 ccatctatcc ttgggataaa cttcttgcca tattttacac tgttttcacc cccatccta 479

<210> 325

<211> 487

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 325

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac 145
 Ala Leu Leu His Thr Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
 35 40 45

cac atc atc tct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ctg 193
 His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga 241
 Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt 289
 Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc 337
 His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
 100 105 110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat 385
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc 433
 Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr

130 135 140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 481
 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ttg 487
 Met Leu

<210> 326
 <211> 162
 <212> PRT
 <213> Pongo pygmaeus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820
 <400> 326
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 327
 <211> 475
 <212> DNA
 <213> Pongo pygmaeus
 <220>
 <221> misc_feature
 <222> (1)..(475)
 <223> Taxon = 9600; gene = PPY119; pseudogene; Accession DDBJ/EMBL/GenBank = AF179821

<400> 327
 gtagccataa gcaaacctct ccactatgca atcatcatga actcatgcac atgtacaggc 60
 ccagtggtag gctcttgggt cattgggggt atgcactccc tgagccagtt agctttcact 120
 gtaagcttgc cttctgtggg cccaaacata gtggacagtt attattgcca cttactttg 180
 gtcacaaac gtgcctgtac agatgcttat atccctgaag tgttgatgct tttggacggc 240
 ggtcttatgg gggtgaccat ttttgctttt gctgatctcc tacacggtca ttctgattac 300
 tgtgcagcga cattcctcag caggatggc caaggctcac agcactctga ctgccacat 360
 tgctgtgggt accgtgttct ttgggccctg tatcttcac tatgcctggc ctttcagcaa 420
 cttaccagtg gataacattt tgtctgtatt ctctgtagtt ttcacaccta tatta 475

<210> 328
 <211> 487
 <212> DNA
 <213> Pongo pygmaeus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9600; gene = PPY120; Accession DDBJ/EMBL/GenBank = AF179822
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 328
 t gtg gcc atc tgt cac cct cta cat tat gcc acc acc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Thr Met Ser Gln Ser
 1 5 10 15

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cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt      97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
      20              25              30

gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac      145
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
      35              40              45

cac atc atc cct cac ttc ttc tgc gac ctt ggt gcc ctg ctc aag ctg      193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
      50              55              60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga      241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
      65              70              75              80

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt      289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
      85              90              95

cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc      337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
      100              105              110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
      115              120              125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
      130              135              140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc      481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
      145              150              155              160

atg ttg      487
Met Leu

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<210> 329

<211> 162

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9600; gene = PPY120; Accession DDBJ/EMBL/GenBank = AF179822

<400> 329

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Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Thr Met Ser Gln Ser
1              5              10              15

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 330

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 330

329

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t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg      49
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1           5           10           15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc      97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
          20          25          30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg cct ttc tgt gat gca      145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala
          35          40          45

aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
          50          55          60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65          70          75          80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
          85          90          95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
          100          105          110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
          115          120          125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
          130          135          140

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145          150          155          160

atg ctg      487
Met Leu

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<210> 331

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<400> 331

330

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
 1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala
 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 332

<211> 488

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9521; gene = SSC185; Accession DDBJ/EMBL/GenBank = AF179824

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 332

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t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg      49
  Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
    1             5             10             15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc      97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
      20             25             30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca      145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
      35             40             45

aac acc gtc cac cac tac ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50             55             60

tcc tgc tca gat atc ttc ctc aac gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85             90             95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
      100            105            110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
      115            120            125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130            135            140

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
      145            150            155            160

atg ctg t
Met Leu
      488

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<210> 333

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9521; gene = SSC185; Accession DDBJ/EMBL/GenBank = AF179824

<400> 333

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
35 40 45

Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 334

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 334

t gtg gcc act tgt cac ccc ctt aga tac atg gtc atc atg aac ccc tgc 49
Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
1 5 10 15

ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat 97
Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
20 25 30

gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat 145
Ala Leu Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt 193
Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
50 55 60

gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct 241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
65 70 75 80

tgc ata ttt ggt ggt gtt cct ctg tct gga atc ata ttc tct tat gct 289
Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
85 90 95

cag att gcc tcc tct att ttg aga atg cca tca gca cgc aga aag tat 337
Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
100 105 110

aaa gcc ttt tcc acc tgt ggg tct cac ctc tcc atg gtg ctc ttg ttc 385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
115 120 125

tat agg aca ggt ttg ggg gtg tac att agt tct gca gtt act gac tca 433
Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
130 135 140

cct agg aag act gca gtg gct tca atg atg tat tct gtg ggt cct caa 481
Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
145 150 155 160

atg gtg 487
Met Val

<210> 335

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<400> 335

Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
1 5 10 15

Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
20 25 30

Ala Leu Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
50 55 60

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
65 70 75 80

Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
85 90 95

Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
115 120 125

Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
130 135 140

Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
145 150 155 160

Met Val

<210> 336

<211> 487

<212> DNA

<213> Saimiri sciureus

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<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC187; Accession DDBJ/EMBL/GenBank = AF179826
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 336
c  gtg gcc atc tgc ctc ccc cta cat tac gcc acc atc atg agc ccc atg      49
  Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
    1              5              10              15

ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
    20              25              30

gcc atg ttg cac act tta ctc atg gcc agg ttg cgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
    35              40              45

aat gtg atc ctc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50              55              60

gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
    65              70              75              80

ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
    85              90              95

cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc      337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
    100             105             110

aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
    115             120             125

tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
    130             135             140

act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc      481
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
    145             150             155             160

atg ctg      487
Met Leu

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<210> 337
<211> 162
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC187; Accession DDBJ/EMBL/GenBank = AF179826
<400> 337

Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
1 5 10 15

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
35 40 45

Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
145 150 155 160

Met Leu

<210> 338


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<211> 487
<212> DNA
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC190; Accession DDBJ/EMBL/GenBank = AF179827
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 338
t gtg gcc atc tgt aag ccc ctg cat tac acc acc atc atg agc agc aaa      49
  Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
    1             5             10             15

atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc      97
  Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
    20             25             30

atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gcc tcc      145
  Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
    35             40             45

aac gtc gtt gat cat ttc tac ttt gac act atc ccg ctc ctg cag att      193
  Asn Val Val Asp His Phe Tyr Phe Asp Thr Ile Pro Leu Leu Gln Ile
    50             55             60

tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tca gcg      241
  Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
    65             70             75             80

ttg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca tat act      289
  Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
    85             90             95

tat att gcc ctg aca att cta aaa atc cct tca act agt cag agg aaa      337
  Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
    100            105            110

aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ctt tct      385
  Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
    115            120            125

tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa caa agg      433
  Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
    130            135            140

gta tct ttt tca aag gga att tcg gtg ctc aat acc tct gtt gct cca      481
  Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
    145            150            155            160

ctt ttg      487
  Leu Leu

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<210> 339
<211> 162
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC190; Accession DDBJ/EMBL/GenBank = AF179827
<400> 339

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
20 25 30

Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
35 40 45

Asn Val Val Asp His Phe Tyr Phe Asp Thr Ile Pro Leu Leu Gln Ile
50 55 60

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
65 70 75 80

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
85 90 95

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
130 135 140

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Leu Leu

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<210> 340
<211> 485
<212> DNA
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF179828
<220>
<221> CDS
<222> (1)..(483)
<223> Product = olfactory receptor
<400> 340
gtg gcc att tgc cac cct ctt caa tac tca gtc atc atg acc aca ggt      48
Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
1          5          10          15

tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc      96
Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
          20          25          30

tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc      144
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
          35          40          45

aat gtt atg aac cac ttt ttc tgt gat atc tca cca gtc cta aaa ctg      192
Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
          50          55          60

gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct      240
Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
65          70          75          80

atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc      288
Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
          85          90          95

tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag      336
Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
          100          105          110

aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt      384
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
          115          120          125

tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca      432
Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
          130          135          140

ttt aat tcc aac aaa cta atg tca gct gtg tat gca gtc ctc aca ccc      480
Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro
145          150          155          160

```

atg ct
Met

485

<210> 341
<211> 161
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF179828
<400> 341

Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
1 5 10 15

Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
20 25 30

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
35 40 45

Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
50 55 60

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
65 70 75 80

Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
85 90 95

Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
130 135 140

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro
145 150 155 160

Met

```

<210> 342
<211> 487
<212> DNA
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC192; Accession DDBJ/EMBL/GenBank = AF179829
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 342
t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg      49
  Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
    1             5             10             15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc      97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
      20             25             30

tcc ctc tct cac acc ctt ctg ctg acc cgg ctg tct ttc tgt gat gca      145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
      35             40             45

aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50             55             60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85             90             95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
      100            105            110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
      115            120            125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130            135            140

```

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc 481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

atg ctg 487
Met Leu

<210> 343
<211> 162
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC192; Accession DDBJ/EMBL/GenBank = AF179829
<400> 343

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 344
 <211> 487
 <212> DNA
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 344
 t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg 49
 Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
 1 5 10 15
 ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc 97
 Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
 20 25 30
 tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca 145
 Ser Leu Ser His Thr Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
 35 40 45
 aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
 Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60
 tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80
 gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95
 tac act ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cgc 337
 Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
 100 105 110
 aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat 385
 Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
 115 120 125
 tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc 433

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc 481
 ile asp lys asp val ile val ala leu thr tyr thr val val thr pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 345

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830

<400> 345

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
 1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser

130

135

140

Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 346
 <211> 486
 <212> DNA
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9521; gene = SSC194; Accession DDBJ/EMBL/GenBank = AF179831
 <220>
 <221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor
 <400> 346
 t gtg gcc atc tgt cac ccc ctg cac tac aca gtc acc att aac ccc aga 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
 1 5 10 15
 ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 97
 Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
 20 25 30
 tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac 145
 Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
 35 40 45
 ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt 193
 Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
 50 55 60
 gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct 241
 Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
 65 70 75 80
 atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct 289
 Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser
 85 90 95
 aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac 337
 Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
 100 105 110
 aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt 385
 Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe

```

115              120              125
tat ggt aca ctc cta ggt gtg tac att agt tct gct gca act ggc aac      433
Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn
130              135              140

tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc      481
Ser His Ser Ser Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
145              150              155              160

atg ct      486
Met

```

```

<210> 347
<211> 161
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9521; gene = SSC194; Accession DDBJ/EMBL/GenBank = AF179831
<400> 347

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Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1              5              10              15

```

```

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20              25              30

```

```

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
35              40              45

```

```

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50              55              60

```

```

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
65              70              75              80

```

```

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser
85              90              95

```

```

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
100              105              110

```

```

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe
115              120              125

```

Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn
 130 135 140

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met

<210> 348
 <211> 487
 <212> DNA
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 348
 c gtg gcc atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag 49
 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
 1 5 10 15
 gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg 97
 Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
 20 25 30
 gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145
 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
 35 40 45
 aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193
 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
 50 55 60
 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg 241
 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
 65 70 75 80
 gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt 289
 Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
 85 90 95
 ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct 337
 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
 100 105 110

```

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc      385
lys ala phe ser thr cys ser ser his ile ile val val ser leu phe
      115                      120                      125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
phe gly ser gly ala phe met tyr leu lys pro pro ser ile leu pro
      130                      135                      140

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc      481
leu asp gln gly lys val ser ser ile phe tyr thr ala val val pro
      145                      150                      155                      160

atg ttt      487
met phe

```

```

<210> 349
<211> 162
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832
<400> 349

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```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1              5              10              15

```

```

Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
      20              25              30

```

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
      35              40              45

```

```

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
      50              55              60

```

```

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val
      65              70              75              80

```

```

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
      85              90              95

```

```

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
      100             105             110

```

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
 115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
 145 150 155 160

Met Phe

<210> 350
 <211> 486
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 27679; gene = SBO213; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF179833
 <400> 350
 cgtggccatc tgccaccctc tccactatcc catccgcatg agtagaagtg tgtgtgtgaa 60
 gatgattgga ggctcttgga cgctgggggc catcaactcc ttggcacaca cagtctatgc 120
 cctccatatt ccctactgca ggtctagagc cattgacccat ttcttctgcg acatcccagc 180
 catgttgctt ctgcctgta cggacacttg ggtctatgaa tacatgggtt ttctaagtac 240
 aagctgcctt ctctcttttc tttccttggc atcacgcgtt cctatggccg agtcctatct 300
 gctgtctacc atacgcatcc aaaaaaggga agaaaaaagg cctccaccac catttcaacc 360
 catttaactg tagtgatctt ttactatgca ccttttgtct acacctatct tcggcccagg 420
 aatctccact caccatccga agacaagatc ctggcagtct tctacaccat ccttaccctt 480
 atgctc 486

<210> 351
 <211> 487
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(487)

<223> Taxon = 27679; gene = SBO214; Accession DDBJ/EMBL/GenBank = AF179834

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 351

t gtg gcc atc tgt aag ccc ctg cat tac acc acc atc atg agc agc aaa 49
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc 97
Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
20 25 30

atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gcc tcc 145
Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
35 40 45

aac gtc gtt gat cat ttc tac tgt gac act atc ccg ctc ctg cag att 193
Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile
50 55 60

tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tca gcg 241
Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
65 70 75 80

ctg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca tat act 289
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
85 90 95

tat att gcc ctg aca att cta aaa atc cct tca act agt cag agg aaa 337
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
100 105 110

aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ctt tct 385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
115 120 125

tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa caa agg 433
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
130 135 140

gta tct ttt tca aag gga att tcg gtg ctc aat acc tct gtt gct cca 481
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
145 150 155 160

ctt ttg 487
Leu Leu

<210> 352

<211> 162

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SB0214; Accession DDBJ/EMBL/GenBank = AF179834

<400> 352

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
20 25 30

Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
35 40 45

Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile
50 55 60

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
65 70 75 80

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
85 90 95

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
130 135 140

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Leu Leu

<210> 353

<211> 487

<212> DNA

<213> Saimiri boliviensis

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<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 353
c gtt gcc att tgc ttc ccc ctt cac tat acg cta ctc atg agc cat tcc      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
    1             5             10             15

att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg      97
  Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
            20             25             30

gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc      145
  Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
            35             40             45

tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg      193
  Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
            50             55             60

gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att ttg ggt      241
  Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
            65             70             75             80

ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct tac gta      289
  Phe Leu Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val
            85             90             95

ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg agg ctc      337
  Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu
            100            105            110

aag tcc ttc tcc acg tgt gct tcc cac gtc act gtg gtc acc atg ttc      385
  Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
            115            120            125

tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac      433
  Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
            130            135            140

cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc tct gcc      481
  Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala
            145            150            155            160

ttc ttg
Phe Leu

```


<210> 354
<211> 162
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835
<400> 354

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
1 5 10 15

Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
20 25 30

Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
35 40 45

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
50 55 60

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
65 70 75 80

Phe Leu Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val
85 90 95

Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu
100 105 110

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
115 120 125

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
130 135 140

Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala
145 150 155 160

Phe Leu

<210> 355

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<211> 487
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO216; Accession DDBJ/EMBL/GenBank = AF179836
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 355
t gtt gcc atc tgc cag ccc ctg cac tac tcc acc ctc ttg agc cca cag      49
  Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Gln
    1             5             10             15

gcc tgc atg acc atg gtg ggc acc tcc tgg ctc aca ggc atc atc aca      97
Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
      20             25             30

gcc acc acc cat gcc tcc ctc atc ttc tct ctg ccc ttc ccc agc cac      145
Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His
      35             40             45

cca atg atc cca cac ttt ctc tgt gac atc ctg cca gta ctg aga ctg      193
Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
      50             55             60

gca agt gct ggg aag cac agg agt gag atc tcc gtg atg aca gct acc      241
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
      65             70             75             80

gta gtc ttc atc atg gtc cct ttc tct atg att gtc acc tct tac atc      289
Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile
      85             90             95

cgc atc ctg ggt gcc atc cta gca atg act tcc acc cag agc cgc cac      337
Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His
      100            105            110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctt gtg gtc tgt ctc ttc      385
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe
      115            120            125

ttt gga aca gcc agc atc acc tac ata cgg ccc cag gca ggc tcc tct      433
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
      130            135            140

gtc acc aca gac cgc atc ctc agt ctc ttc tac acg gtc atc aca ccc      481
Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
      145            150            155            160

atg ctc      487
Met Leu

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<210> 356
<211> 162
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO216; Accession DDBJ/EMBL/GenBank = AF179836
<400> 356
Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Gln
1 5 10 15

Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
20 25 30

Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His
35 40 45

Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
50 55 60

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
65 70 75 80

Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile
85 90 95

Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His
100 105 110

Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe
115 120 125

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
130 135 140

Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
145 150 155 160

Met Leu

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<210> 357
<211> 487
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AF179837
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 357
t gtg gcc att tgc cac ccc ctc tac tac tcc aca gtc atg agc ccc caa      49
Val Ala Ile Cys His Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
1          5          10          15

gtc tgt gcc cta atc ctc gtg ttg tgc tgg gtc ctc acc aac gtt gtt      97
Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val
20          25          30

gcc ttg acc cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act      145
Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
35          40          45

ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta      193
Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
50          55          60

tca tgt tct gac acc cac atc aat gag atg atg gtt ttt gtc ttg gga      241
Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
65          70          75          80

ggc aca gta ctc atc atc ccc ttt cta tgc att gtc acc tcc tac atc      289
Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
85          90          95

tac att gtg cct gct att ctg agg gtc cga acc cat ggt ggg gcg ggc      337
Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
100         105         110

aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt gtg ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
115         120         125

tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tcc atc gcc tct      433
Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130         135         140

gaa gat aag gac att gca aca gct gca atg tat acc ata gtg act ccc      481
Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
145         150         155         160

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acg ttg
Thr Leu

487

<210> 358
<211> 162
<212> PRT
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AF179837
<400> 358
Val Ala Ile Cys His Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
1 5 10 15

Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val
20 25 30

Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
35 40 45

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
65 70 75 80

Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
85 90 95

Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130 135 140

Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
145 150 155 160

Thr Leu

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<210> 359
<211> 486
<212> .DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838
<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor
<400> 359
c gtg gct atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag      49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
  1             5             10             15

gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg      97
Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
      20             25             30

gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa      145
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
      35             40             45

aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc      193
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
      50             55             60

tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg      241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val
      65             70             75             80

gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt      289
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
      85             90             95

ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
      100            105            110

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
      115            120            125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
      130            135            140

```

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg cca 481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
145 150 155 160

tgt tt 486
Cys

<210> 360

<211> 161

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838

<400> 360

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1 5 10 15

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
20 25 30

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
35 40 45

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
50 55 60

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val
65 70 75 80

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
85 90 95

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
 145 150 155 160

Cys

<210> 361
 <211> 487
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO219; Accession DDBJ/EMBL/GenBank = AF179839
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor
 <400> 361
 t gtg gcc att tgc cac cct ctt caa tac tca gtc atc atg acc aca ggt 49
 Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
 1 5 10 15
 tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc 97
 Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
 20 25 30
 tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc 145
 Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
 35 40 45
 aat gtt atg aac ctc ttt ttc tgt gat atc tca cca gtc cta aaa ctg 193
 Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
 50 55 60
 gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct 241
 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
 65 70 75 80
 atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc 289
 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
 85 90 95
 tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag 337
 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
 100 105 110
 aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt 385
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
 115 120 125
 tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca 433

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
130 135 140

ttt aat tcc aac aaa cta atc tca gct gtc tat gca gtc ctc aca ccc 481
Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro
145 150 155 160

atg cta 487
Met Leu

<210> 362

<211> 162

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO219; Accession DDBJ/EMBL/GenBank = AF179839

<400> 362

Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
1 5 10 15

Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
20 25 30

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
35 40 45

Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
50 55 60

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
65 70 75 80

Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
85 90 95

Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser

130

135

140

Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro
145 150 155 160

Met Leu

<210> 363
<211> 488
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 27679; gene = SB0220; pseudogene; Accession DDBJ/EMBL/GenBank = AF179840
<400> 363
tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcctgca 60
gcttgctgctt ggggtgctggg ttcttggttt tctcatcatc tttccaccac tcctcttagg 120
actaaatctt gacttctgtg cctccaacgt cgttgatcat ttctactgtg aactatccc 180
gtcctgcag atttcctgca cagacacgca gtcctggag aggatgggat tcatctcagc 240
gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgcct 300
gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc 360
tcacatgatt gtgatatccc ttcttatgg cagctgccat cttcatgtat gttaagccat 420
cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc 480
cacttttg 488

<210> 364
<211> 487
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SB0221; Accession DDBJ/EMBL/GenBank = AF179841
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 364

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c  gtg gcc atc tgc ctc ccc cta cat tac gcc acc atc atg agc ccc atg      49
  Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
  1              5              10              15

ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
      20              25              30

gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
      35              40              45

aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
      50              55              60

gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
      65              70              75              80

ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
      85              90              95

cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc      337
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
      100              105              110

aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc      385
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
      115              120              125

tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
      130              135              140

act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc      481
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
      145              150              155              160

atg ctg      487
Met Leu

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<210> 365

<211> 162

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO221; Accession DDBJ/EMBL/GenBank = AF179841

<400> 365

Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
 1 5 10 15

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
 35 40 45

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
 130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
 145 150 155 160

Met Leu

<210> 366

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO222; Accession DDBJ/EMBL/GenBank = AF179842

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 366

c gtg gcc atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag 49

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln

1 5 10 15

gtg tgt ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg 97

Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly

20 25 30

gct gtg gct cat aca gga aat ata gtg ttt cta acc ttt tgt gca ggc 145

Ala Val Ala His Thr Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Gly

35 40 45

aac ctt gtc aat cac tac atg tgt gac atc ctt ccc ctt ctt gag ctc 193

Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu

50 55 60

tcc tgc aat ggc tct tac ata aat gtt ctg gtc atc ttt att gtt gtg 241

Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val

65 70 75 80

acc att ggc att ggg gtg ccc att gtt gcc att ttt atc tct tat ggt 289

Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly

85 90 95

ttt att ctt tcc agc aat ctc cac att agt tct gct gag ggc agg tct 337

Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser

100 105 110

aaa gcc ttc agt acc tgc agc tcc cac ata att gca gtt tct ctt ttc 385

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe

115 120 125

ttc ggg tca gga gct ttt atg tac ctc aaa ccc tct tcc gtt tta ccc 433

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro

130 135 140

ctg gac cag ggg aaa gta tcc tcc ctg ttt tat act att gtg gtg ccc 481

Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro

145 150 155 160

atg ttt 487

Met Phe

<210> 367

<211> 162

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO222; Accession DDBJ/EMBL/GenBank = AF179842

<400> 367

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1 5 10 15

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
20 25 30

Ala Val Ala His Thr Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Gly
35 40 45

Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
50 55 60

Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val
65 70 75 80

Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly
85 90 95

Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe
115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro
130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro
145 150 155 160

Met Phe

<210> 368

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

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<222> (1)..(487)
<223> Taxon = 27679; gene = SBO223; Accession DDBJ/EMBL/GenBank = AF179843
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 368
t gtg gcc atc tgt cac ccc ctg cac tac aca gtc acc att aac ccc aga      49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
    1             5             10             15

ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat      97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
      20             25             30

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac      145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
      35             40             45

ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt      193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
      50             55             60

gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct      241
Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
      65             70             75             80

atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct      289
Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser
      85             90             95

aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac      337
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
      100            105            110

aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt      385
Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe
      115            120            125

tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac      433
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
      130            135            140

tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc      481
Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
      145            150            155            160

atg ctg
Met Leu
      487

<210> 369
<211> 162

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<212> PRT
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO223; Accession DDBJ/EMBL/GenBank = AF179843
 <400> 369

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
 1 5 10 15

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
 20 25 30

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
 35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
 50 55 60

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
 65 70 75 80

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser
 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
 130 135 140

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 370

<211> 649

<212> DNA
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank = AF073959
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
 <400> 370
 c ata gct gac atc ggc ttc acc tcc acc act atc ccc aag gtt ctg cag 49
 Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln
 1 5 10 15
 act atc cac aca cag agc aaa ttc atc tct ttc tcg ggc tgc atc aca 97
 Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr
 20 25 30
 cag ata ttt ttc ttc att gtg ttt gga tgc ctg gac aat tta ctc cta 145
 Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45
 tca gtg atg gcc tat gac cgc ttt gtg gcc atc tgc cat ccc ttg cac 193
 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tat gtg gtc atc atg aat tct tgc ttc tgt gtg atg ctg gct ctt gga 241
 Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly
 65 70 75 80
 tca tgg ata gtc agc gtc atg agt tcc cta cct gag acc ttg act gtg 289
 Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val
 85 90 95
 tta aga cta tcc ttc tgt aca aac atg gaa att cca cac ttt ttc tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 gat ctt ccc gaa gtc ctg aag ctt gcc tgt tct gac acc ctt gtt aat 385
 Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn
 115 120 125
 aac att gtg aca tat tct ata acc ata gtc ata gct ggt ttc cca ttc 433
 Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe
 130 135 140
 tct ggg att cta ttg tct tat tct aag att ttc tcc tcc atc cta aga 481
 Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160
 att cct tca gct ggg ggc aag tac aaa gcc ttt tct acc tgt ggg tct 529

```

Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
      165                      170                      175

cat ctt ttg gtg gtc ttc tta ttc tat agc aat ggt ctt ggg gtc tac      577
His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr
      180                      185                      190

ctc agc tct gca gcc aca tca tct tct aga atg agt cta gtt gcc tca      625
Leu Ser Ser Ala Ala Thr Ser Ser Arg Met Ser Leu Val Ala Ser
      195                      200                      205

ctg atg tac agc ata gtc act ccc      649
Leu Met Tyr Ser Ile Val Thr Pro
      210                      215

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<210> 371
<211> 216
<212> PRT
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank =
AF073959
<400> 371

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Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln
1              5              10              15

```

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Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr
      20              25              30

```

```

Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu Leu
      35              40              45

```

```

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50              55              60

```

```

Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly
      65              70              75              80

```

```

Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val
      85              90              95

```

```

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
      100              105              110

```

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn
115 120 125

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe
130 135 140

Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg
145 150 155 160

Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser
195 200 205

Leu Met Tyr Ser Ile Val Thr Pro
210 215

<210> 372

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank =

AF073960

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7

<400> 372

c ttc tct gac ttc tgc ttt tcc tct gtg acc att ccc aaa ttg ctg cag 49
Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1 5 10 15

aac atg caa agc caa gtt cca tcc ata ccc tat gca ggt tgc ctg gca 97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

caa atg tac ttt ttc ctg ctt ttt gca gat ctc gag agc ttc ctc ctt 145
Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu
35 40 45

```

gtg gcc atg gcc tat gat cgc tat gtg gcc atc tgc ttc ccc cta cac      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
    50                      55                      60

tat act agc atc atg agc ccc aag ctg tgt ctc tgc ctg gtg gca cta      241
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu
    65                      70                      75                      80

tct tgg cta ctg acc aca gtc atc tct ttg tca cac aca ctg ctc atg      289
Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met
                      85                      90                      95

gct cgg ctc tcc ttc tgt gct aac aat gtg att cct cac ttt ttc tgt      337
Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
                      100                      105                      110

gat atg tca gct ctt ctg aag tta gcc tgc tct gac att cag atc aat      385
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn
                      115                      120                      125

aag ttg atg ata ttt atc ttg gga gga ctt gtc att att gtc cca ttc      433
Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe
    130                      135                      140

ctg ctg ata ttt tca tcc tat gca cga ata gtg tcc tcc att ctc aag      481
Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
    145                      150                      155                      160

gtc ccc tct tct aga agc atc cgc aag gcc ttc tcc acc tgt ggt tcc      529
Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
                      165                      170                      175

cac ctc tct gtg gtg tct ctt ttc tat ggg aca atc att ggt ctc tat      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
                      180                      185                      190

tta cgt cca tca gct aat aat tca acc att aag gag act gtc atg gct      625
Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala
                      195                      200                      205

gtg atg tac acg gtg gtg acc cct      649
Val Met Tyr Thr Val Val Thr Pro
    210                      215

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<210> 373
<211> 216
<212> PRT
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)

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<223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank =
AF073960

<400> 373

Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu
65 70 75 80

Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met
85 90 95

Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn
115 120 125

Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe
130 135 140

Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180 185 190

Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

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<210> 374
<211> 649
<212> DNA
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7
<400> 374
c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag      49
  Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
    1             5             10             15

aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca      97
Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
    20             25             30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
    35             40             45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
    50             55             60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg      241
Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
    65             70             75             80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg      289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
    85             90             95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt      337
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
    100            105            110

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat      385
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
    115            120            125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt      433
Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
    130            135            140

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gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag 481
 Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc 529
 Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cac ctg tct gtg gtg tca ctg ttc tat ggg gca atc att ggt ctg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr
 180 185 190

tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc 625
 Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
 195 200 205

atg atg tac aca gtg gtg act ccc 649
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 375

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961

<400> 375

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
 115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 376

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 376

t ttc tct gac ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

aat atg cag agc cag gac cca tcc atc ccc tat gga ggt tgc ctg gca 97
 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala
 20 25 30

caa ata ttc ttc ttt atg ctt ttt gga gac atg gaa agc ttc ctt ctt Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45	145
gta gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60	193
tac act agc atc atg agt cct aag gtc tgt act ttt cta gtg cta ctg Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu 65 70 75 80	241
ttg tgg ata ctg aca aca cca cat gcc aca atg caa att ctg ctc aca Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr 85 90 95	289
gta aga ctg tct ttt tgt gag aac aat gtg ttt ctc aac ttt ttc tgt Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys 100 105 110	337
gac ata ttt gtt ctc tta aag ctg gcc tgc tca gac act tat gtt aat Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125	385
gat ttg atg ata ctt atc atg gga ggg ctc atc att gtt att cca ttc Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130 135 140	433
ctg ctc att gtt ata tcc tat gca agg atc atc tcc tct act ctt aag Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145 150 155 160	481
gtt cca tct act caa ggc atc cac aag gtc ttc tct acc tgt ggc tct Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175	529
cat ctg tct gtg gtg tct ctg ttc tat ggg aca att att ggt ctc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	577
tta tgt cca tca ggt aat aat ttc agt cta aag ggg tct gcc atg gct Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala 195 200 205	625
atg atg tac aca gtg gtg act ccc Met Met Tyr Thr Val Val Thr Pro 210 215	649

<210> 377

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<400> 377

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala
20 25 30

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu
65 70 75 80

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr
85 90 95

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys
100 105 110

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
115 120 125

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe
130 135 140

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys
145 150 155 160

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala

195

200

205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 378
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
 <400> 378
 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg cta cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15
 aac atg cag agc cag gac acg tcc atc tcc tat gct ggc tgt ctg aca 97
 Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 caa atg tac ttt tta ttg gtt ttt gga gac ctg gag agc atc ctt ctt 145
 Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu
 35 40 45
 ttg gtc atg gct tat gac cgg tat gtg gct gtc tgc ttc ccc ctt cat 193
 Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His
 50 55 60
 tac atg agc atc atg agc ccc aca ctc tgt gtg tgt ctg cta gtg tta 241
 Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu
 65 70 75 80
 tcc tgg gta ttt act gtg ctg tat tct atg ttg cac act cta ctc ttg 289
 Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu
 85 90 95
 tct aga ttg tca ttc tgt gag gat aac ttg atc cac cac ttt ttc tgt 337
 Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys
 100 105 110
 gac ata tct gcc ctg ctc aag ttg gct tgc tct gac att cat att aat 385
 Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
 115 120 125
 gaa tta atg ata ttt atc atg gga ggg ctt gtt agc atc atc cca ttc 433

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe
 130 135 140

tta ctc att gtt gtg tcc tat ata caa att gtc tac tcc att cta aag 481
 Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys
 145 150 155 160

att tca tct gct cat gtt tta cac aag atc ttc tcc acc tgt ggg tcc 529
 Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser
 165 170 175

cac ctg tct gta gtc tca ctg ttc tat ggg aca att ttt gct ctc tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr
 180 185 190

tta tgt cca tca gct aat aac tct act gtg aag gag att tcc atg gcc 625
 Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala
 195 200 205

atg atg tgc aca gtg gtg act ccc 649
 Met Met Cys Thr Val Val Thr Pro
 210 215

<210> 379
 <211> 216
 <212> PRT
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963
 <400> 379
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu
 35 40 45

Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His
 50 55 60

Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu
 65 70 75 80

Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu

WO 01/46262

381

PCT/IB00/02017

85

90

95

Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe
130 135 140

Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys
145 150 155 160

Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr
180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala
195 200 205

Met Met Cys Thr Val Val Thr Pro
210 215

<210> 380

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank =
AF073964

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7

<400> 380

c ttt tct gac att ggt ttc atc tct aca act atc cct aag atg ttg gtg 49
Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
1 5 10 15

aat atc caa aca cag agc aag tcc atc tcc tat gca gaa tgc atc acc 97
 Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
 20 25 30

cag att tat ttt ttc atg ctc ttt gga ggc atg gac ata ctt ctc ctc 145
 Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu Leu
 35 40 45

acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctt cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tat tca gtc att atg aat ccc caa cta agt ggc ttg ctg gtt ctt gta 241
 Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
 65 70 75 80

tca tgg ttt att agc ttt tca tat tct ctg ata cag agt cta ttg atg 289
 Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
 85 90 95

ctg cgg ttg tcc ttc tgt aca aat cag ata att aaa cac ttt tac tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
 100 105 110

gaa tat tct aga gcc ctc act ata gcc tgc tca gac aca cta atc aat 385
 Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
 115 120 125

cat atc ctt ctt tat att ctg ata tgt gtc ctt ggc ttc atc cct ttc 433
 His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
 130 135 140

tca ggg atc ctt tat tca tac tgt aaa att gtt tct tct att ttg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

att cca tca aca gat gga aaa tat aaa gca ttt tct acc tgt ggg tct 529
 Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

cat cta tca gtg gtt tct tta ttc tat ggg aca ggc ctt ggt gtg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

ctt agt tct gat gta act tcc tcc tct ggg aag gac gtg gtg gcc tca 625
 Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser
 195 200 205

gta atg tat aca gtg gtc acc cct 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<211> 216
<212> PRT
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank =
AF073964
<400> 381
Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
20 25 30

Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
100 105 110

Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
115 120 125

His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

180

185

190

Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 382

<211> 643

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank =
 AF073965

<220>

<221> CDS

<222> (2)..(643)

<223> Product = olfactory receptor; region between transmembrane domains TM2
 and TM7

<400> 382

g ttc gta gat ctc tgc ttc tca tcc gtc acg gta ccg aaa ctg ctg aag 49
 Phe Val Asp Leu Cys Phe Ser Ser Val Thr Val Pro Lys Leu Leu Lys
 1 5 10 15

gac ctc cta tcg gcg aag aaa acc atc tca ata gaa ggc tgc ctg gct 97
 Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala
 20 25 30

cag gtc ttt ttt gtg ttt ttt cct tct ggt act gaa gcc tgc ctg ctc 145
 Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu
 35 40 45

tct gtc atg gct tat gac cgc tat gct gcc atc tgc cat ccc ctg ctc 193
 Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu
 50 55 60

tac ggc cag gtg atg aga aat gag ttg tgt gta agg ctt gtg gtc atc 241
 Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile
 65 70 75 80

tca tgg ggc gtg gcc tct ctc aac gca acc atc atc gtg ctc ttg gct 289
 Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala
 85 90 95

gtc aac ctg gac ttc tgt ggg gct caa acc att cac cac tac acc tgt 337
 Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys
 100 105 110


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gag ctg cct gcc ctt ttc ccc ttg tcc tgt tcc gat atc tcc atc act      385
Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr
      115                      120                      125

gtc gtc gtc ctg ctt tgc tcc agc ttg ctg cat ggg ctg gga acc ttt      433
Val Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe
      130                      135                      140

atc cct atc ttc ttc tcc tat gcc cgc att gtc tcc gcc atc ttg agc      481
Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser
      145                      150                      155                      160

atc agt tcc acc acc ggg agg agc aag gcc ttc tcc acc tgc tct tcc      529
Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
      165                      170                      175

cac ctg gct gca gtg acc ttg ttc ttt ggg tct ggc ttt ctt tgc tat      577
His Leu Ala Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr
      180                      185                      190

ctc atg ccg cct tct ggt tct tct ctg gac ttg ctc ttg tgc ttg cag      625
Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Leu Ser Leu Gln
      195                      200                      205

tac agc gca gtc acg ccc      643
Tyr Ser Ala Val Thr Pro
      210

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<210> 383

<211> 214

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank = AF073965

<400> 383

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Phe Val Asp Leu Cys Phe Ser Ser Val Thr Val Pro Lys Leu Leu Lys
1              5              10              15

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Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala
      20              25              30

```

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Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu
      35              40              45

```

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Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu
      50              55              60

```

Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile
65 70 75 80

Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala
85 90 95

Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys
100 105 110

Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr
115 120 125

Val Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe
130 135 140

Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser
145 150 155 160

Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ala Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr
180 185 190

Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Leu Ser Leu Gln
195 200 205

Tyr Ser Ala Val Thr Pro
210

<210> 384

<211> 643

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =
AF073966

<220>

<221> CDS

<222> (2)..(643)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 384

```

c ctt gtt gac atc ttc ttc tcc tct gta act att ccc aag atg ctg gcc      49
  Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
    1             5             10             15

aac cat ctc cta ggt agc aag gcc atc tcc ttt ggg gga tgt atg gca      97
Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
    20             25             30

cag atg tac ttc atg ata tca ttg gga aac aca gac agt tat ata cta      145
Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
    35             40             45

gct gca atg gca tat gac cga gct gtg gct atc agt cgc ccg ctt cat      193
Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
    50             55             60

tat gca aca att atg agt cca caa ctt tgt gtc ctg ctg gtt gct ggg      241
Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
    65             70             75             80

tcc tgg gtg att gca aat gct aat gca ctg ccc cac acc cta ctc aca      289
Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
    85             90             95

gct aga ttg tcc ttc tgt ggc aat aag gat gtg gcc aac ttc tac tgt      337
Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
   100             105             110

gac att aca cct ttg ctc cag ctg tcc tgt tct gac atc cgc ttc aat      385
Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
   115             120             125

gtg aag atg atg tac ctt ggg gtg ggg gtc ttc tct gtg cca ctg ctg      433
Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
   130             135             140

tgc atc atc atc tcc tat gtc cgg gtc ttt tcc aca gtc ttg cgg gtt      481
Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
   145             150             155             160

cca tct acc aag ggc ttc ctg aag gcc ttg tcc acc tgt ggc tct cac      529
Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
   165             170             175

ctg aca gtg gtg tcc ttg tat tat ggg aca gtc atg ggc atg tat ttc      577
Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
   180             185             190

cgg ccc ctg acc agt tac agt ctg aag cat gca ttg ata act gtg atg      625
Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
   195             200             205

```

tac acg gca gtg acc cca
Tyr Thr Ala Val Thr Pro
210

643

<210> 385
<211> 214
<212> PRT
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =
AF073966
<400> 385

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
1 5 10 15

Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
20 25 30

Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
35 40 45

Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
50 55 60

Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
65 70 75 80

Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
85 90 95

Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
100 105 110

Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
115 120 125

Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
130 135 140

Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
145 150 155 160

Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
 165 170 175

Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
 180 185 190

Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
 195 200 205

Tyr Thr Ala Val Thr Pro
 210

<210> 386

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 386

c ctg gtg gac atc tgc ttt acc act gtc atc gtg cca cag atg tta gtg 49
 Leu Val Asp Ile Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val
 1 5 10 15

aac ttg ctg aca cag aga aag aca atc ctc ttt gcc cag tgc ctc act 97
 Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr
 20 25 30

caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg 145
 Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu
 35 40 45

gct gcg atg gcc att gac cgc tat gtt gct att tgc aat ccg ctt cat 193
 Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His
 50 55 60

tac aac aca gtc atg agt ccc agg cgc tgt cgc ttg ctg gtt gtg gca 241
 Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala
 65 70 75 80

tcc tgg gca gtg tcc cat ctt cac tcc ctc acc cac aca att ctc atg 289

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met
85 90 95

ggt cgc ctc tct ttc tgt gga ccc aat gtc att cat cac ttc ttt tgt 337
Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys
100 105 110

gat gtc cag cca ctg ctg aca ctc tcc tgc tct gac acc tct atc aat 385
Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn
115 120 125

gag ctc ttg gcc ttc aca gag ggc tct gtt gta atc atg agc cct ttt 433
Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe
130 135 140

atc tta ttg ttg tct ctt ata tct ata ttc act cgg act gtt ctg agg 481
Ile Leu Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg
145 150 155 160

gtc cct tca ggg gaa gga agg tac aaa gtt ttc tct acc tgt ggg tct 529
Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

cac ctc aca gtt gta gca ctg ttc tat gga acc ata ata tca gtg tac 577
His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr
180 185 190

att cgc ccc tca tcc acc tac tca gtg aca aag gac cga gtt gtc act 625
Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr
195 200 205

gtc atc tat aca gta gtt acc cca 649
Val Ile Tyr Thr Val Val Thr Pro
210 215

<210> 387

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967

<400> 387

Leu Val Asp Ile Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val
1 5 10 15

Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu
 35 40 45

Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His
 50 55 60

Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala
 65 70 75 80

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met
 85 90 95

Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys
 100 105 110

Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn
 115 120 125

Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe
 130 135 140

Ile Leu Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg
 145 150 155 160

Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr
 180 185 190

Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr
 195 200 205

Val Ile Tyr Thr Val Val Thr Pro
 210 215

<210> 388

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)
 <223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7
 <400> 388
 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

 aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca 97
 Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
 20 25 30

 caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt ctt 145
 Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
 35 40 45

 gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa 193
 Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
 50 55 60

 tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg ttc 241
 Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
 65 70 75 80

 tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg 289
 Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
 85 90 95

 gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt 337
 Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110

 gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat 385
 Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
 115 120 125

 gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc 433
 Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
 130 135 140

 tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg 481
 Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

 att tct tct act cgg gct atc cat aag ctc ttc tcc acc tgt ggc tca 529
 Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
 165 170 175

 cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr


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                180                185                190
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
                195                200                205

ctg atg tac aca gtg gtg act ccc      649
Leu Met Tyr Thr Val Val Thr Pro
                210                215

<210> 389
<211> 216
<212> PRT
<213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968
<400> 389
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1                5                10                15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
                20                25                30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
                35                40                45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
                50                55                60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
65                70                75                80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
                85                90                95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
                100                105                110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
                115                120                125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
                130                135                140

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Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 390

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR1M; Accession DDBJ/EMBL/GenBank = AF073969

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 390

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca 97
 Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt 145
 Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
 35 40 45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta 241
 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu

65	70	75	80	
ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca				289
Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala				
	85	90	95	
gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt				337
Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys				
	100	105	110	
gac cta ttt gtt ctc cta aag ctg gct tgc tca gac act tat gtt aat				385
Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn				
	115	120	125	
gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt				433
Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe				
	130	135	140	
ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag				481
Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys				
	145	150	155	160
gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc				529
Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser				
	165	170	175	
cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac				577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr				
	180	185	190	
tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc				625
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala				
	195	200	205	
atg atg tac aca gtg gtg act ccc				649
Met Met Tyr Thr Val Val Thr Pro				
	210	215		

<210> 391

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR1M; Accession DDBJ/EMBL/GenBank = AF073969

<400> 391

Phe	Ser	Asp	Leu	Cys	Phe	Ser	Ser	Val	Thr	Met	Pro	Lys	Leu	Leu	Gln
1				5					10				15		

Asn	Ile	Gln	Ser	Gln	Asp	Pro	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ala
		20						25					30		

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
 65 70 75 80

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
 100 105 110

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
 115 120 125

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe
 130 135 140

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 392

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

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<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR21M; Accession DDBJ/EMBL/GenBank = AF073970
<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7
<400> 392
c ttt gca gac atc tgc ttt act tct gct agc atc cca aag atg cta gtg      49
  Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val
    1             5             10             15

aat ata cag aca aag aac aag gtg ata acc tat gaa ggt tgc att tct      97
Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser
      20             25             30

caa gta ttc ttt ttc ata cta ttt gga gtt tta gat aac ttt ctt cta      145
Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu
      35             40             45

gct gtg atg gcc tat gac cga tat gtg gca atc tgt cac cct ctg cac      193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50             55             60

tat atg gtc atc atg aac cgc cgc ctc tgt gga ttt tta gtt ttg ggg      241
Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly
      65             70             75             80

tct tgg gtc aca aca gca ttg aat tcc ttg ctg cag agt tca atg gca      289
Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala
      85             90             95

ctg cgg ctg tcc ttt tgt aca gac ttg aaa att ccc cac ttt gtt tgt      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys
      100            105            110

gag ctt aat caa ctg gta cta ctt gcc tgt aat gac acc ttt cct aat      385
Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn
      115            120            125

gac atg gtg atg tac ttt gca gct ata ctg ctg ggt ggt ggt cct ctt      433
Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu
      130            135            140

gct ggc atc ctt tac tct tat tct aag ata gtt tcc tcc ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
      145            150            155            160

atc tca tca tca cag ggg aag tat aaa gca tcc tcc acc tgt gca tcc      529
Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser
      165            170            175

cac ctc tca gtt gtt tca tta ttc tat tct aca ctc ttg ggt gcg tat      577

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His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
 180 185 190

ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca tct 625
 Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser
 195 200 205

gtt atg tac agt gtg gtc acc ccc 649
 Val Met Tyr Ser Val Val Thr Pro
 210 215

<210> 393

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR21M; Accession DDBJ/EMBL/GenBank = AF073970

<400> 393

Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser
 20 25 30

Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly
 65 70 75 80

Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys
 100 105 110

Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn
 115 120 125

Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu
 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
 180 185 190

Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser
 195 200 205

Val Met Tyr Ser Val Val Thr Pro
 210 215

<210> 394

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 394

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca 97
 Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
 20 25 30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145
 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg 241
 Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg 289
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95

 gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc tac ttt ttc tgt 337
 Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
 100 105 110

 gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat 385
 Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
 115 120 125

 gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt 433
 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140

 gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag 481
 Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

 gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc 529
 Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

 cac ctg tct gtg gtg tca ctg ttc tat ggg aca atc att ggt ctg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

 tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc 625
 Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
 195 200 205

 atg atg tac aca gtg gtg act ccc 649
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 395

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<400> 395

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
65 70 75 80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
130 135 140

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 396

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 396

c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49
Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
1 5 10 15

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97
Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

caa atg tac ttc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt 145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
35 40 45

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat 193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241
Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65 70 75 80

tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289
Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt 337
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat 385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt 433
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa 481
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
145 150 155 160

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg tct 529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac 577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180 185 190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct 625
Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
195 200 205

atg atg tac act gtg gtg att ccc 649
Met Met Tyr Thr Val Val Ile Pro
210 215

<210> 397

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972

<400> 397

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65 70 75 80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
 180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
 195 200 205

Met Met Tyr Thr Val Val Ile Pro
 210 215

<210> 398

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 398

c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49
 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
 1 5 10 15

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97
 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
 35 40 45

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
 50 55 60

tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241
 Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
 65 70 75 80

tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt 337
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat 385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt 433
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc act ctc aaa 481
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys
145 150 155 160

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct 529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac 577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180 185 190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct 625
Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
195 200 205

atg atg tac act gtg gtg act ccc 649
Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 399
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973
<400> 399
Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
50 55 60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65 70 75 80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 400

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 400

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a gtg gtg gac atc tgc tac acc tcc agt ggg gtc ccc cag atg ctg gca      49
  Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala
    1             5             10             15

cac ttc ctc atg gag aaa aag acc atc tct ttt gcc cta tgt ggg acc      97
His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr
      20             25             30

cag ctc ttc ttt gct ctg act ctt ggg gga act gag ttt ctg ttg ctg      145
Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu Leu
      35             40             45

act gcc atg gcc tat gac cgc tat gtg gct gtc tgt aat cca tta cgg      193
Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg
      50             55             60

tac aca gtg gtg atg aac cca agg ctc tgc atg ggt cta gca ggt gtc      241
Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val
      65             70             75             80

tct tgg ttt gtg ggt gta gtt aat tct gct gtg gag aca gca gtc acc      289
Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr
      85             90             95

atg tac ctt ccc acc tgt ggg cac aat gta ctc aac cat gtg gcc tgt      337
Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys
      100            105            110

gag aca ctg gca ctg gtc aga ctg gcc tgt gtg gac atc acc ctc aac      385
Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn
      115            120            125

caa gtg gtg ata ctg gct tct agt gtg gtg gtg ctg atg ata ccc tgc      433
Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys
      130            135            140

tct ctg gtc tct ctg tcc tat gcc cac att gta gct gcc atc atg aag      481
Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys
      145            150            155            160

atc cgt tct acc cag gga cgc cgc aaa gcc ttt gag acc tgt gcc tcc      529
Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser
      165            170            175

cat ctg act gtg gtc tcc atg tct tat ggg atg gcc ctc ttc acc tac      577
His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr
      180            185            190

ctg cag cct gcc tcc aca gcc tct gct gag cag gac aag gtg gta gtg      625

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Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val
195 200 205

atc ttc tat gct ttg gtc acc ccc
ile phe tyr ala leu val thr pro
210 215

649

<210> 401

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974

<400> 401

Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala
1 5 10 15

His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr
20 25 30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu Leu
35 40 45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg
50 55 60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val
65 70 75 80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr
85 90 95

Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys
100 105 110

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn
115 120 125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys
130 135 140

Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys
145 150 155 160

Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser
 165 170 175

His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr
 180 185 190

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val
 195 200 205

Ile Phe Tyr Ala Leu Val Thr Pro
 210 215

<210> 402

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 402

t ttc gtt gac ctc tgc cag tcc agt gtc atc atg ccc aaa atg ctg gag 49
 Phe Val Asp Leu Cys Gln Ser Ser Val Ile Met Pro Lys Met Leu Glu
 1 5 10 15

aaa ttt gtc atg gtg aag agt gtc att tct ttt gca gaa tgc atg gct 97
 Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala
 20 25 30

cag ttt tac tta ttt gat gtt ttt gct gtt tca gag tgt cac atg ctg 145
 Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu
 35 40 45

gct gtc atg gct tat gat cgc tat gtt gcc atc tgt aac ccc ttg cta 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu
 50 55 60

tat aat gtt acc atg tct tac aaa gtg tgt tcc tgg atg gta gtg ggg 241
 Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly
 65 70 75 80

gtg tat agt gta gcc ttg att tgt gcc aca ggg gaa aca gtc tgc ctg 289
 Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu
 85 90 95

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ctt aga ctg cta ttc tgc aaa gct gat gac ata aac cac tac ttc tgt      337
Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys
      100              105              110

gat ctt tta cca cta ctg gaa caa tcc tgt tcc aat aca ttt atc aat      385
Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn
      115              120              125

gaa ata cta gga ctg tcc ttc agt tca ttt aat act act gtc cca gct      433
Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala
      130              135              140

ctg acc atc ctc agt tcc tac atc ttc atc ata gcc agc atc ctc cgc      481
Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg
      145              150              155              160

att cct tcc act gaa ggc agg tcc aaa gcc ttc agc acc tgc agc tcc      529
Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
      165              170              175

cac atc ttg gct gtt gct gtc ttc ttt ggg tct tta gca ttc atg tac      577
His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr
      180              185              190

ctt cag cca tca tca gtc agc tcc atg gac caa ggg aaa gtg tcc tct      625
Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser
      195              200              205

gtg ttt tat acc att gtt gtg ccc      649
Val Phe Tyr Thr Ile Val Val Pro
      210              215

<210> 403
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975
<400> 403
Phe Val Asp Leu Cys Gln Ser Ser Val Ile Met Pro Lys Met Leu Glu
1              5              10              15

Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala
      20              25              30

Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu
      35              40              45

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Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu
50 55 60

Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly
65 70 75 80

Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu
85 90 95

Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys
100 105 110

Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn
115 120 125

Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala
130 135 140

Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg
145 150 155 160

Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr
180 185 190

Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser
195 200 205

Val Phe Tyr Thr Ile Val Val Pro
210 215

<210> 404

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 404

c ttc act gac ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag	49
Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln	
1 5 10 15	
aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca	97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr	
20 25 30	
caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt	145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu	
35 40 45	
gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat	193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His	
50 55 60	
tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg	241
Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu	
65 70 75 80	
tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta	289
Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu	
85 90 95	
act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt	337
Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys	
100 105 110	
gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat	385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn	
115 120 125	
gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt	433
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe	
130 135 140	
cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag	481
Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys	
145 150 155 160	
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct	529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser	
165 170 175	
cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac	577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr	
180 185 190	
tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct	625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser	
195 200 205	

ctg atg tac act gtg gta act ccc
Leu Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 405
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976
<400> 405
Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 406

<211> 650

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(650)

<223> Taxon = 10092; clone = OR3M; Accession DDBJ/EMBL/GenBank = AF073977

<220>

<221> CDS

<222> (3)..(650)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 406

cc ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg 47
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
 1 5 10 15

cag aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg 95
 Gln Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu
 20 25 30

aca caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt 143
 Thr Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu
 35 40 45

ctt gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt 191
 Leu Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu
 50 55 60

caa tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg 239
 Gln Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val
 65 70 75

ttc tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc 287
 Phe Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu
 80 85 90 95

ttg gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc 335

Leu Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe
 100 105 110

tgt gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att 383
 Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile
 115 120 125

aat gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc acc tca 431
 Asn Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Thr Ser
 130 135 140

ctc tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta 479
 Leu Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu
 145 150 155

agg att tct tct act cgg gct atc cat aag ctc ttc tcc acc tgt ggc 527
 Arg Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly
 160 165 170 175

tca cac ctg tct gtg gtc tca ctg ttc tat ggg gca att att ggt ctg 575
 Ser His Leu Ser Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu
 180 185 190

tac tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg 623
 Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met
 195 200 205

tcc ctg atg tac aca gtg gtg act ccc 650
 Ser Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 407
 <211> 216
 <212> PRT <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(650)
 <223> Taxon = 10092; clone = OR3M; Accession DDBJ/EMBL/GenBank = AF073977
 <400> 407

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Thr Ser Leu
130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
195 200 205

Leu Met Tyr Thr Val Val Thr Pro
210 215

<210> 408

<211> 648

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 408

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag	49
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln	
1 5 10 15	
aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca	97
Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr	
20 25 30	
caa atg tac ttt ttc agt gtt ttt ggg agt ctg gag ata ttc ctt ctt	145
Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu	
35 40 45	
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa	193
Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln	
50 55 60	
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg ttc	241
Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe	
65 70 75 80	
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg	289
Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu	
85 90 95	
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt	337
Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys	
100 105 110	
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat	385
Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn	
115 120 125	
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc	433
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu	
130 135 140	
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg	481
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg	
145 150 155 160	
att tct tct act cgg gct atc cat aag ctc ttc tcc acc tgt ggc tca	529
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser	
165 170 175	
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac	577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr	
180 185 190	
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc	625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser	
195 200 205	
ctg atg tac aca gtg gtg act cc	648

Leu Met Tyr Thr Val Val Thr
210 215

<210> 409

<211> 215

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<400> 409

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr
 210 215

<210> 410

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank = AF073979

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 410

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca 97
 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr
 20 25 30

caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt 145
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu
 35 40 45

gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat 193
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc 241
 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu
 65 70 75 80

tct tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg 289
 Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu
 85 90 95

gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt 337
 Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110

gac ata tct gcc ctg ctc aag ttg gcc tgc tct gac att tct att aat 385
Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn
115 120 125

gaa cta atg ata ttt atc gtg gga ggg ctt gat act gta atc cca ttt 433
Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe
130 135 140

tta	ctc	att	gtt	gtt	tcc	tat	gta	caa	att	gtc	tgc	tcc	att	cta	aag	481
Leu	Leu	Ile	Val	Val	Ser	Tyr	Val	Gln	Ile	Val	Cys	Ser	Ile	Leu	Lys	
145					150					155					160	

ttc tca tct aca cgg ggc ata cac aag gtc ttc tcc acc tgt ggc tcc 529
Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt gtc tac 577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
180 185 190

ata tgc cca tca gct aat aac tct act gtg aag gag act gtc atg tcc 625
Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser
195 200 205

ctg atg tac aca gtg gtg acg ccc 649
Leu Met Tyr Thr Val Val Thr Pro
210 215

<210> 411

<211> 216

<212> PRT <213> Mus musculus domesticus

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<221> misc_feature
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<222> (1) .. (649)

<223> Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank = AF073979

<400> 411

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu
35 40 45

Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu
65 70 75 80

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu
85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn
115 120 125

Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe
130 135 140

Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys
145 150 155 160

Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
180 185 190

Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser
195 200 205

Leu Met Tyr Thr Val Val Thr Pro
210 215

<210> 412

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 412

c ttc act gac ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag

Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Gln	
1 5 10 15	
aac atg cag agc caa gtt cct tca atc ccc tat gca gcc tgc ctg aca	97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr	
20 25 30	
caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt	145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu	
35 40 45	
gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat	193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His	
50 55 60	
tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg	241
Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu	
65 70 75 80	
tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta	289
Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu	
85 90 95	
act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt	337
Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys	
100 105 110	
gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat	385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn	
115 120 125	
gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt	433
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe	
130 135 140	
cta ctc gtc aca gtg cct tat gca cgc atc atc tcc tcc att ctc aag	481
Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys	
145 150 155 160	
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct	529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser	
165 170 175	
cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac	577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr	
180 185 190	
tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct	625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser	
195 200 205	
ctg atg tac act gtg gta act ccc	649
Leu Met Tyr Thr Val Val Thr Pro	
210 215	

<210> 413
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980
<400> 413
Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 414

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 414

c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49
 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
 1 5 10 15

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97
 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agc tta ctc ctt 145
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
 35 40 45

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241
 Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
 65 70 75 80

tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289
 Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
 85 90 95

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt 337
 Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat 385

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
 115 120 125
 gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt 433
 Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
 130 135 140
 cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa 481
 Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
 145 150 155 160
 gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct 529
 Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 cat ctg tct gcg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac 577
 His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
 180 185 190
 tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct 625
 Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
 195 200 205
 atg atg tac act gtg gtg act ccc 649
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 415

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981

<400> 415

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
 1 5 10 15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu

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65

70

75

80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 416

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 416

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

1	5	10	15	
aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca				97
Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala				
20	25	30		
caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt				145
Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu				
35	40	45		
gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat				193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His				
50	55	60		
tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta				241
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu				
65	70	75	80	
ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca				289
Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala				
85	90	95		
gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt				337
Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys				
100	105	110		
gac cta ttt gta ctc cta aag ctg gct tgc tca gac act tat gtt aat				385
Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn				
115	120	125		
gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt				433
Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe				
130	135	140		
ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag				481
Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys				
145	150	155	160	
gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc				529
Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser				
165	170	175		
cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac				577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr				
180	185	190		
tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc				625
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala				
195	200	205		
atg atg tac aca gcg gtg act ccc				649
Met Met Tyr Thr Ala Val Thr Pro				
210	215			

<210> 417
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982
<400> 417
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
65 70 75 80

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
85 90 95

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
100 105 110

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
115 120 125

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe
130 135 140

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

180

185

190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Ala Val Thr Pro
 210 215

<210> 418
 <211> 649
 <212> DNA <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR912-47M4; Accession DDBJ/EMBL/GenBank =
 AF073983
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2
 and TM7
 <400> 418
 c ttt gtg gac atc tgt ttt acc tcc acc act gtc cca aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc 97
 Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
 20 25 30
 cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg 145
 Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
 35 40 45
 gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca tta tat 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
 50 55 60
 tac aca gtc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg 241
 Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
 65 70 75 80
 tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gtg 289
 Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
 85 90 95
 cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgt 337
 Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
 100 105 110
 gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc ttt tca agc 385

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser
 115 120 125
 caa ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc 433
 Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
 130 135 140
 agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct 481
 Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
 145 150 155 160
 atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct 529
 Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175
 cac ctt tcc att gtc tcc tta ttt tat agt aca ggc ctt gga gtg tat 577
 His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
 180 185 190
 gtc agt tct gtt gtg atc caa agc tct cac tct gct gca aga gcc tct 625
 Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser
 195 200 205
 gtg atg tat act gtg gtc acc ccg 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 419

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

 <223> Taxon = 10092; clone = OR912-47M4; Accession DDBJ/EMBL/GenBank =
 AF073983

<400> 419

 Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

 Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
 20 25 30

 Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
 35 40 45

 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
 50 55 60

Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

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65	70	75	80
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val	85	90	95
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys	100	105	110
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser	115	120	125
Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe	130	135	140
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser	145	150	155
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser	165	170	175
His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr	180	185	190
Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser	195	200	205
Val Met Tyr Thr Val Val Thr Pro	210	215	

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<210> 420
<211> 646
<212> DNA <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank =
AF073984
<220>
<221> CDS
<222> (2)..(646)
<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7
<400> 420
c tct gtg gat gta tgc ttc tcc tcc acc act gtc cct aag gta ctg gcc

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6

<210> 421
<211> 215
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank =
AF073984
<400> 421

Ser Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
1 5 10 15

Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
20 25 30

Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly
65 70 75 80

Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val
85 90 95

Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys
100 105 110

Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
115 120 125

Glu Leu Met Ile Leu Ala Val Ala Gly Leu Ile Met Leu Ala Pro Phe
130 135 140

Val Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ala Cys Ala Ile Leu Lys
145 150 155 160

Ile Ser Ser Thr Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His
165 170 175

Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ser Leu Tyr Phe
 180 185 190

Asn Pro Ser Ser Ser His Ser Ala Gly Arg Asp Met Ala Ala Ala Met
 195 200 205

Met Tyr Thr Val Val Thr Pro
 210 215

<210> 422

<211> 650

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(650)

<223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/ GenBank =
 AF073985

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
 and TM7

<400> 422

c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Thr Ser Thr Val Pro Lys Met Leu Val
 1 5 10 15

aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc 97
 Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
 20 25 30

cag atg tct gtc ttc ttg gtt ttt gga gaa ctg gac aac ttt ctc ctg 145
 Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn Phe Leu Leu
 35 40 45

gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
 50 55 60

tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg 241
 Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
 65 70 75 80

tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gta 289
 Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
 85 90 95

cta cag ttg acc ttt tgt gga gat gta aga att ccc cac ttc ttc tgt 337
 Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys

100	105	110	
gag ctt aac cag ctg tct caa ctc aca tgt tca gac agc tta tca agc			385
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Leu Ser Ser			
115	120	125	
cac ctc ata atg cat ctt gta cct gtt cta ttg gga gcc att tcc ttc			433
His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala Ile Ser Phe			
130	135	140	
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct			481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser			
145	150	155	160
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct			529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser			
165	170	175	
cac ctt tcc att gta tcc tta ttt tat agt aca ggc ctt gga gtg tat			577
His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr			
180	185	190	
gtc agt tct gct gtg gtc caa agc tct cac tct gct gca aga gcc tct			625
Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser			
195	200	205	
gtg atg tat act gtg gtc aca cac g			650
Val Met Tyr Thr Val Val Thr His			
210	215		

<210> 423

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(650)

<223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/ GenBank = AF073985

<400> 423

Phe	Val	Asp	Ile	Cys	Phe	Thr	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Val
1				5					10					15	

Asn	Ile	Gln	Thr	Gln	Ser	Lys	Ala	Ile	Thr	Tyr	Ala	Asp	Cys	Ile	Ser
		20					25						30		

Gln	Met	Ser	Val	Phe	Leu	Val	Phe	Gly	Glu	Leu	Asp	Asn	Phe	Leu	Leu
	35					40						45			

Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Tyr
	50					55				60					

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
65 70 75 80

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
85 90 95

Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Leu Ser Ser
115 120 125

His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala Ile Ser Phe
130 135 140

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
145 150 155 160

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
165 170 175

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
180 185 190

Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr His
210 215

<210> 424

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR912-47M8; Accession DDBJ/EMBL/GenBank =
AF073986

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 424

c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag gtg ctg gta	49
Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Val Leu Val	
1 5 10 15	
aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc	97
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser	
20 25 30	
cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg	145
Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu	
35 40 45	
gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat	193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr	
50 55 60	
tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg	241
Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu	
65 70 75 80	
tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gtg	289
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val	
85 90 95	
cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgc	337
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys	
100 105 110	
gag ctt aac cag ctg tct caa ctc aca tgt tta gac agc ttt tca agc	385
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser	
115 120 125	
cac ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc	433
His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe	
130 135 140	
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct	481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser	
145 150 155 160	
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct	529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser	
165 170 175	
cac ctt tcc att gtc ttc tta ttt tat agt aca ggc ctt gga gtg tat	577
His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr	
180 185 190	
gtc agt tct gct gtg gtc caa agc tct cac tct gct gca aga gcc tct	625
Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser	
195 200 205	

gtg atg tat act gtg gtc acc ccg
Val Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 425
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR912-47M8; Accession DDBJ/EMBL/GenBank =
AF073986
<400> 425
Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Val Leu Val
1 5 10 15

Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
20 25 30

Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
50 55 60

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
65 70 75 80

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
85 90 95

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser
115 120 125

His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
130 135 140

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
145 150 155 160

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175

His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
 180 185 190

Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 426

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR912-47M9; Accession DDBJ/EMBL/GenBank =
 AF073987

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
 and TM7

<400> 426

c ttt gca gat ctc tgc ttt tct act acc aca gtg ccc cag gtg ctt gtc 49
 Phe Ala Asp Leu Cys Phe Ser Thr Thr Thr Val Pro Gln Val Leu Val
 1 5 10 15

cac ttc ctg gtg aag agg aag acc att tct ttt gct gga tgt tct aca 97
 His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr
 20 25 30

cag ata gtg gtg ttg ctt ctg gtc gga tgc aca gag tgt gca ctg ctg 145
 Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu
 35 40 45

gca gtg atg tcc tat gac cga tat gtg gct gtc tgc aaa cct ctg cac 193
 Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His
 50 55 60

tac tcc acc atc atg aca cac tgg cta tgt gtt cag ctg gct gca ggg 241
 Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly
 65 70 75 80

tcc tgg gcc agt ggt gca ctt gtg tcc ctg gtg gat acc aca ttc aca 289
 Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr
 85 90 95

tta cgt ctt cct tat cga gga aac aat gtc att aac cac ttt ttc tgt 337
 Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys
 100 105 110
 gaa cct cct gcc ctc ctg aag ctg gca tcg gca gat aca tac agc aca 385
 Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr
 115 120 125
 gag atg gcg atc ttt gca atg ggt gtg gta atc ctc cta gca cct gtc 433
 Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val
 130 135 140
 tcc ctc atc ctc acc tcc tac tgg aac atc atc tcc act gta atc cag 481
 Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln
 145 150 155 160
 atg cag tct ggg gaa gga agg ctc aag gtc ttc tcc acc tgt ggc tcc 529
 Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 cac ctc att gtt gtt gtt ctc ttc tac ggc tca gca ata ttt gcc tac 577
 His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr
 180 185 190
 atg agg ccc aac tct aag ata atg aat gaa aag gat aaa atg att tcg 625
 Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser
 195 200 205
 gtg ttc tat tca gca gtg acc ccg 649
 Val Phe Tyr Ser Ala Val Thr Pro
 210 215

<210> 427

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

 <223> Taxon = 10092; clone = OR912-47M9; Accession DDBJ/EMBL/ GenBank =
 AF073987

<400> 427

 Phe Ala Asp Leu Cys Phe Ser Thr Thr Thr Val Pro Gln Val Leu Val
 1 5 10 15

 His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr
 20 25 30

 Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu
 35 40 45

Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His
 50 55 60

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly
 65 70 75 80

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr
 85 90 95

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys
 100 105 110

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr
 115 120 125

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val
 130 135 140

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln
 145 150 155 160

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr
 180 185 190

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser
 195 200 205

Val Phe Tyr Ser Ala Val Thr Pro
 210 215

<210> 428

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 428

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c ttc act gac ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag      49
  Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
    1             5             10             15

aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca      97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
      20             25             30

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
      35             40             45

gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50             55             60

tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg      241
Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
      65             70             75             80

tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta      289
Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
      85             90             95

act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt      337
Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
      100            105            110

gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat      385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
      115            120            125

gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt      433
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
      130            135            140

cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag      481
Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
      145            150            155            160

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct      529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
      165            170            175

cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
      180            185            190

tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser

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195 200 205 649
ctg atg tac act gtg gta act ccc
Leu Met Tyr Thr Val Val Thr Pro
210 215

<210> 429
<211> 216
<212> PRT <213> Mus musculus domesticus
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988
<400> 429
Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 430

<211> 1865

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(1865)

<223> Taxon = 10090; clone = OR1-72M13; cell line = NIH3T3; Accession
 DDBJ/EMBL/GenBank = AF073989

<220>

<221> CDS

<222> (547)..(1482)

<223> Product = olfactory receptor; orthologous to human gene OR1-72

<400> 430

ctgcagagtg agttcttagga cagccaggac tacacagaga aacctgaat caaaataaaa 60
 taaaataaaa tacaatagaa taaaataaaa taaacaaaaa agaaaaaga agataaagat 120
 gtctaagaga agaagagat ttcaaaagga atggatacag agaaggtatg gtcattattca 180
 cagagacctt tctgaatgat cagaacttag tgtaaccact gaaaaatgtt gagaagtga 240
 gttggaaatc agagttgatc catcataaag gattacagca cttttagaaa ctgactgctt 300
 tgatctaaca ctccagagg ttatctggtc ttcattgtgt tttaaatttg tagagttagc 360
 agttctaagt agagataagg tagagaaact aataatgatg agaaaatgca ggattcctaa 420
 tttttattgt aataaaagct ttatgtacag ttattccaac acataaaagg acagagacct 480
 tagagactgt agtgtatggt cctcaatctt tctctccagt aggtgtctag cttatttgc 540
 aacaac atg aaa cca gaa aac caa aca aaa tat ttt aga att ttt gct 588
 Met Lys Pro Glu Asn Gln Thr Lys Tyr Phe Arg Ile Phe Ala
 1 5 10
 tct ggg gtt ttc caa tat cca gag cat caa ccc atg cta ttt gga ctg 636
 Ser Gly Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu

15	20	25	30	
ttt ctg ctc atg ttt gtg gtc gct gtg ctt ggg aat ctt ctc atc att				684
Phe Leu Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile				
35		40	45	
ctg gcc gtc agc att gac tct cac ctg cat act ccc atg tac ttc ttt				732
Leu Ala Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe				
50		55	60	
cta tct aac ctg tcc ttt tct gac att ggt ttc atc tct aca act gtc				780
Leu Ser Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val				
65		70	75	
cct aag atg ttg gtg aat atc caa aca cag agc aag tcc atc tcc tat				828
Pro Lys Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr				
80		85	90	
gca gaa tgc atc acc cag att tat ttt ttc atg ctc ttt gga ggc atg				876
Ala Glu Cys Ile Thr Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met				
95	100	105	110	
gac aca ctt ctc ctc acc gtg atg gcc tat gac cga ttt gtg gcc atc				924
Asp Thr Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile				
115		120	125	
tgt cac cca ctt cac tat tca gtc att atg aat cct caa cta agt ggt				972
Cys His Pro Leu His Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly				
130		135	140	
ttg cta gtt ctt gta tca tgg ttt att agc ttt tca tat tct ctg ata				1020
Leu Leu Val Leu Val Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile				
145		150	155	
cag agt cta ttg atg ctg cgg ttg tcc ttc tgt aca aat cag ata att				1068
Gln Ser Leu Leu Met Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile				
160		165	170	
aaa cac ttt tac tgt gaa tat gcc aaa gcc ctc act ata gcc tgc tca				1116
Lys His Phe Tyr Cys Glu Tyr Ala Lys Ala Leu Thr Ile Ala Cys Ser				
175	180	185	190	
gat aca cta atc aat cat atc ctt ctt tat att gtg ata tgg gtc ctt				1164
Asp Thr Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu				
195		200	205	
ggc ttc atc cct ttc tca ggg atc ctt tat tca tac tat aaa att ttt				1212
Gly Phe Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe				
210		215	220	
tct tca att ttg aga att cca tca aca gat gga aaa tat aaa gca ttt				1260
Ser Ser Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe				
225		230	235	

tct acc tgt ggg tct cat cta tcg gtg gtt tct tta ttc tat ggg aca 1308
 Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr
 240 245 250

ggc ctt agt gtg tac ctt agt tct gat gct act tcc tcc tct ggg aag 1356
 Gly Leu Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys
 255 260 265 270

ggc gtg gtg gcc tca gta atg tat aca gtg gtc acc ccc atg ctg aac 1404
 Gly Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285

cct ttc atc tac agc ttg agg aac aaa gac att aag aag gcc tta aaa 1452
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys
 290 295 300

aca ctt ggg aga ata ctt ctt tta aag tga taatttcact ggtttttagac 1502
 Thr Leu Gly Arg Ile Leu Leu Leu Lys
 305 310

atctgaactg atagaaataa aatagtgaac taaagaaatt ctgtactata atcatgtaga 1562

aattttatcc agtttggttg tctatctttg attaaaatta tactgtgaat atttctatct 1622

gaaatttcta tgatgcctcc ttttttattc gaagtctttt gtctcctccc ctgttttata 1682

cgacatatatt ctttacttca gtacaaagtc tacatttcag catgcccaata taaccattca 1742

aataccaatt catgaattgt ttagtaaaaag ttatgcaatg gctcatttac agaaagtcca 1802

tgtatatata tataaactg ttgtgggttg gtccgactct gtattctgat attaattctg 1862

cag 1865

<210> 431

<211> 311

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(1865)

<223> Taxon = 10090; clone = OR1-72M13; cell line = NIH3T3; Accession
 DDBJ/EMBL/GenBank = AF073989

<400> 431

Met Lys Pro Glu Asn Gln Thr Lys Tyr Phe Arg Ile Phe Ala Ser Gly
 1 5 10 15

Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu Phe Leu
 20 25 30

Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45

Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60

Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val Pro Lys
65 70 75 80

Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu
85 90 95

Cys Ile Thr Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Thr
100 105 110

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
115 120 125

Pro Leu His Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu
130 135 140

Val Leu Val Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser
145 150 155 160

Leu Leu Met Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His
165 170 175

Phe Tyr Cys Glu Tyr Ala Lys Ala Leu Thr Ile Ala Cys Ser Asp Thr
180 185 190

Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe
195 200 205

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser
210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
245 250 255

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PCT/IB00/02017

Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys Gly Val
260 265 270

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys Thr Leu
290 295 300

Gly Arg Ile Leu Leu Leu Lys
305 310